

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Nita M Minnifield

Location: rem-3c01/3c18

Art Unit: 1644

Tuesday, April 04, 2006

Case Serial Number: 09/942098

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524







STIC-Biotech/ChemLib

183919

From:

Chan, Christina

Sent:

Monday, April 03, 2006 8:11 AM

To: Subject: Minnifield, Nita; STIC-Biotech/ChemLib RE: rush interference sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From:

Minnifield, Nita

Sent:

Monday, April 03, 2006 7:48 AM

To:

Chan, Christina

Subject:

rush interference sequence search

Christina,

Please approve, 2 month amdt. due.

STIC

09/942098

Please do an interference sequence search on SEQ ID NO: 1, 2, 30, and aa 187-203 of SEQ ID NO: 2 of this application.

Please do a commercial and interference sequence search on SEQ ID NO: 29, 90-93 and aa 191-202 of SEQ ID NO: 2 of this application.

Please provide a paper printout of all results.

Thanks, Minnifield

Searcher:	
Searcher Phone:	
Date Searcher Picked up:_	
Date completed:	
Searcher Prep Time:	
Online Time:	

*****	*****									
Type	of Search									
NA#	_ AA#:									
S/L: Oligomer:										
Encode/Tran										
Structure #:	Text:									
Inventor:	Litigation:									

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
www/Internet:
Other (Specify):

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Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence

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US-10-948-097-36 US-10-948-097-40 US-10-948-097-41 US-10-948-097-4 US-10-947-071-4 US-10-947-071-2 US-10-948-097-2 US-10-948-097-2 US-10-948-097-2 US-10-948-097-2 US-10-948-097-2 US-10-948-097-20 US-10-948-097-20 US-10-948-097-20 US-10-948-097-20 US-10-948-097-20 US-10-948-097-20 US-10-948-097-61 US-10-948-097-61 US-10-948-097-61 US-10-948-097-61 US-10-948-097-61 US-10-948-097-61

1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0

Sequence Sequence Sequence Sequence

ALIGNMENTS

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

- protein search, using sw model OM protein

(without alignments) 235.925 Million cell updates/sec April 3, 2006, 15:23:07 ; Search time 1.03226 Seconds Run on:

US-09-942-098-1 39 Title: Perfect score:

1 EANQRATK 8

BLOSUM62 Scoring table: Sequence:

180808 segs, 30441898 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA New:*

1: /SIDSS/ptodata/1/pubpaa/USO8 NEW FUB.pep:*

2: /SIDSS/ptodata/1/pubpaa/USO6 NEW FUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/USO7 NEW FUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/USO9 NEW FUB.pep:*

6: /SIDSS/ptodata/1/pubpaa/USIO_NEW_FUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/USIO_NEW_FUB.pep:*

8: /SIDSS/ptodata/1/pubpaa/USIO_NEW_FUB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	App1	Appli	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl						
ឌ្គ	22,	22,	30,	30,	31,	31,	32,	32,	, ,		33,	34,	20,	51,	62,	33,	34,	50,	51,	62,	35,	35,	36,	40,	41,
Description	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence		Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence						
	947-071-22	948-097-22	947-071-30	948-097-30	947-071-31	948-097-31	0-947-071-32	948-097-32	-086	980-346B-37	947-071-33	10-947-071-34	10-947-071-50	10-947-071-51	10-947-071-62	10-948-097-33	10-948-097-34	US-10-948-097-50	10-948-097-51	10-948-097-62	10-947-071-35	948-097-35	US-10-947-071-36	US-10-947-071-40	-10-947-071-41
ΙD	6	US-10-	US-10-	US-10-	US-10-	us-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-
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* Query Match Length DB	8	80	13	13	15	15	16	16	17	17	17	17	17	17	17	17	17	17	17	17	18	18	33	33	33
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
Result No.	-	8	e	4	ß	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25



US-10-947-071-22

| Sequence 22, Application US/10947071
| Publication No. US20060063221A1
| Publication No. US20060063221A1
| Publication No. US20060063221A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Dudley J.
| APPLICANT: Steward, Lance
| APPLICANT: Steward, Lance
| APPLICANT: Steward, Lance
| APPLICANT: Acki, Kei Roger
| TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
| TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
| TITLE OF INVENTION: For Determining Clostridial Toxin Activity
| FILE REFERENCE: 66872-043
| CURRENT APPLICATION NUMBER: US/10/947,071
| CURRENT FILING DATE: 2004-09-21
| NUMBER OF SEQ ID NOS: 100
| WINDER OF SEQ ID NOS: 400 SEQ ID NO 22

ö Length 8; 0; Indels 100.0%; Score 39; DB 6; I 100.0%; Pred. No. 1.4e+05; 0; Mismatches Conservative Best Local Similarity Matches 8; Conserv Query Match

OTHER INFORMATION: synthetic construct

US-10-947-071-22

FEATURE:

ORGANISM: Artificial Sequence

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Gaps

1 EANORATK 8

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Sequence 22, Application US/10948097
; Bublication No. US20060063222A1
; GENERAL INFORMATION:
 APPLICANT: Williams, Dudley J.
 APPLICANT: Glimore, Marcella
 APPLICANT: Glimore, Marcella
 APPLICANT: Acki, Kei Roger
 TITLE OF INVENTION: Fluorescence Polarization Assays For
 TITLE OF INVENTION: Determining Clostridial Toxin Activity
 FILE REFERENCE: 66972-040
 CURRENT APPLICATION NUMBER: US/10/948,097 RESULT 2 US-10-948-097-22

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Gaps
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APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: Lonchanide-Based Substrates and Methods
TITLE OF INVENTION: Por Determining Clostridial Toxin Activity
FILE REPERENCE: 66872-643
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT APPLICATION DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PASTSEQ for Windows Version 4.0
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Sequence 31, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REPERBUES: 6697-040

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT APPLICATION NUMBER: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 31

LENGTH: 15
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100.0%; Score 39; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                              Query Match 100.0%; Score 39; DB 6; Length 13; Best Local Similarity 100.0%; Pred. No. 0.0052; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10947071 Publication No. US20060063221A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-947-071-31
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US-10-948-097-31
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   US-10-948-097-30
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LENGTH: 15
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US-10-947-071-30
US-10-947-071-30
Sequence 30, Application US/10947071
Publication No. US20060063221A1
Sequence 30, Application US/2060063221A1
APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: AoAt, Kei Roger.
TITLE OF INVENTION: Lethanide-Based Substrates and Methods
CURRENT APPLICANTON NOWBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER C, SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LEASTH: 13
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: APPLICANT: Almore, Marcella

APPLICANT: APPLICANT: Almore, Marcella

APPLICANT: APPLICANT: Almore, Marcella

APPLICANT: APPLICANT: Almore, Marcella

APPLICANT: Almore, Marc
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100.0%; Score 39; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
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100.0%; Pred. No. 1.4e+05;
ative 0; Mismatches 0;
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 8
                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
FATURE INFORMATION: synthetic construct
US-10-948-097-22
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Best Local Similarity 100.
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-947-071-30
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ORGANISM: Homo sapiens
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8 EANORATK 15
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LENGTH: 17
                                                                               SEQ ID NO 6
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Sequence 32, Application US/10947071

Fublication No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Ackingen, Marcella

APPLICANT: Ackingen, Marcella

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: For Determining Clostridial Toxin Activity

FILE REPRENCE: 66872-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT PILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFUMARE: PastSEQ for Windows Version 4.0

SEQ ID NO 32

LENGTH: 16
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APPLICANT: Verhagen, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Greward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REPERENCE: 66872-007
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 39; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/10990346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
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; Sequence 32, Application US/10948097
; Publication No. US/2060063222A1
; GENERAL INFORMATION:
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Matches 8; Conservative
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US-10-948-097-32
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US-10-947-071-32
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"US-10-30-346B-37
"US-10-30-346B-37
"Sequence 37, Application US/10980346B
"Sequence 37, Application US/10980346B
"Publication No. US20060024763A1
"GENERAL INFORMATION:
"APPLICANT: Los Alamos National Laboratory
"APPLICANT: Schmidt, Jurgen G., et al.
"TITLE OF INVENTION: Ass Spectrometry-Based Methods for Detection and Differentiation
"TITLE OF INVENTION: of Botulinum Neurotoxins
"TITLE OF INVENTION: of Botulinum Neurotoxins
"TITLE OF INVENTION WIMBER: US/10/980,346B
"CURRENT FILING DATE: 2044-11-03
"NUMBER OF SEQ ID NOS: 55
"SOFTWARE: Patentin version 3.2
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation TITLE OF INVENTION: of Botulinum Neurotoxins FILE REFERENCE: S-102,313 CURRENT APPLICATION NUMBER: US/10/980,346B CURRENT APPLICATION DATE: 2004-11-03 NUMBER OF SEQ ID NOS: 55 SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum OTHER INFORMATION: Neurotoxin (BONT)
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum OTHER INFORMATION: Neurotoxin (BONT)
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Publication No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Achingen, Marc

APPLICANT: Achi, Kei Roger

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: For Determining Clostridial Toxin Activity
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100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: amide bound at one end of the peptide US-10-980-346B-37
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: synthetic construct US-10-947-071-50
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ORGANISM: Artificial Sequence
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LOCATION: 16

CTHER INFORMATION: Xaa=Nle

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LENGTH: 17
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; Publication No. US20060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Steward, Lance
; APPLICANT: Steward, Lance
; APPLICANT: Steward, Lance
; APPLICANT: Action Marcella
; APPLICANT: Action Marcella
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: Lanthanide-Based Substrates
; TITLE OF INVENTION: Lanthanide Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICANTON NUMBER: US/10/947,071
; CURRENT PILLING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FREUSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENDTH: 17
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US-10-947-071-34

Squence 34, Application US/10947071

Publication No. US2060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Glimore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Verhagen, Marc

APPLICANT: Acki, Kei Rogen

TITLE OF INVENTION: Earthanide-Based Substrates and Methods

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: Each Determining Clostridial Toxin Activity

FILE REPERRUE: 66872-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT PILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 17
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Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 17
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; ORGANISM: Homo sapiens
US-10-947-071-33
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ORGANISM: Homo sapiens
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Sublication No. US20060063221A1

Sublication No. US20060063221A1

SUBLICANT: Williams, Dudley J.

APPLICANT: Gilmore, Marcella

APPLICANT: Glemach, Lance

APPLICANT: Activated, Lance

APPLICANT: Activated Roger

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: For Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFTHARE: FREESE for Windows Version 4.0
                                                                                                                                                                                                                                                                                              Sequence 51. Application US/10947071
; Sequence 51. Application US/2060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Steward, Lance
; APPLICANT: Steward, Lance
; APPLICANT: Acki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT FALIGE APPLE 2004-09-21
; WINNERS FILIGE DATE: 2004-09-21
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100.0%; Score 39; DB 6; Length 17; 100.0%; Pred. No. 0.0071; vative 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: synthetic construct US-10-947-071-62
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0; Gaps Query Match 100.0%; Score 39; DB 6; Length 17; Best Local Similarity 100.0%; Pred. No. 0.0071; Matches 8; Conservative 0; Mismatches 0; Indels

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Search completed: April 3, 2006, 15:27:30 Job time: 1.03226 secs

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Sequence 1, Application US/09942098
; Bequence 1, Application No. US20030143651A1
; GENERAL INFORMATION:
    APPLICANT: Steward, Lance E.
    APPLICANT: Fernandez-Salas, Ester
    APPLICANT: Poxins
    TITLE OF INVENTION: Toxins
    FILE REFERENCE: P-AR 4802
    CURRENT APPLICATION NUMBER: US/09/942,098
    CURRENT PILING DATE: 2001-08-28
    NUMBER OF SEQ ID NOS: 96
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 1
    LENGTH: B
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Sequence 1,
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *

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US-10-317-844-1

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US-10-917-842-161-49

US-10-917-842-088-28

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US-09-942-024-45
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Maximum Match 100%
Listing first 45 summaries
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Publication No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward. Lance E.
APPLICANT: Peranadez-Salas, Ester
APPLICANT: Peranadez-Salas, Ester
TITLE OF INVENTION: Fret Frotease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 201-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PastSEQ for Windows Version 4.0

SEQUINO 1
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100.0%; Score 39; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0;
US-09-942-024-56
US-09-942-098-30
US-09-942-098-31
US-09-942-098-45
US-09-942-098-45
US-09-942-098-65
US-09-942-098-65
US-00-011-598-56
US-10-261-161-52
US-10-261-161-68
US-10-261-161-69
US-10-261-161-69
US-10-261-161-81
US-10-261-161-81
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US-10-261-161-81
US-10-261-161-81
US-10-917-844-31
US-10-917-844-44
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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US-09-942-098-27
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                                                                     RESULT 5
US-10-917-844-1
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LENGTH: 8
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US-10-261-161-41
Sequence 41, Application US/10261161
Sequence 41, Application No. US2040072270A1
Sequence 41, Application No. US20040072270A1
GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: PAR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 8
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GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Evolved Clostridial Toxins With Altered; TITLE OF INVENTION: Protease Specificity; FILE REFERENCE: P-AR 4670; CURRENT APPLICATION WUMBER: US/10/318,417; CURRENT FILING DATE: 2002-12-11; NUMBER OF SEQ ID NOS: 12; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
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                                                                                                                                                                             Query Match 100.0%; Score 39; DB 3; Length 8; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 8; Conservative 0; Mismatches 0; Indels
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100.0%; Score 39; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                     CTHER INFORMATION: synthetic construct US-09-942-098-1
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ORGANISM: Artificial Sequence
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                                          FEATURE:
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100.0%; Score 39; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels
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Publication No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance B.
APPLICANT: Farmander-Salae, Ester
APPLICANT: Farmander-Salae, Ester
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Fret Protease Assays
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQUENCE: SALES OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 39; DB 5; Length 13; 100.0%; Pred. No. 0.22; Aztive 0; Mismatches 0; Indels

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Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
; ORGANISM: Homo sapiens
US-10-917-844-27
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US-09-942-024-28
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| Sequence 27, Application No. US20050100973A1
| Publication No. US20050100973A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. APPLICANT: Gilmore, Marcella A. APPLICANT: Gilmore, Marcella A. TITLE OF INVENTION: For Botulinum Neurotoxin Protease Assay TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity; FILE REFERENCE: 66872-044
| CURRENT APPLICATION NUMBER: US/10/917,844
| CURRENT FILING DATE: 2001-08-28
| NUMBER OF SEQ ID NOS: 113
| SEQ ID NO 27
| LENGTH: 13
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Publication No. US2004007227041

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxi

FILE REFERENCE: P-48 4804

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEC ID NOS: 109

SOFTWARE: PastSEQ for Windows Version 4.0

SED ID NO 49

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  APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Free Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
SED IN NO 27
LENGTH: 13
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-09-942-098-27
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ORGANISM: Homo sapiens
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Sequence 66, Application US/20040072270A1

Publication No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT APPLICATION UNDEBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 66

LENGTH: 15
Sequence 50, Application US/10261161
; Sequence 50, Application US/20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Acki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050100973A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Glimore, Marcella A.

APPLICANT: Aoki, Kei R.

TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay

TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity

FILE REFERENCE: 66872-044

CURRENT APPLICATION NUMBER: US/10/917,844
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 8; Conservative
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/ ORGANISM: Homo sapiens
US-10-261-161-50
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US-10-917-844-28
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LENGTH: 15
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100.0%; Score 39; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels
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| Sequence 29, Application US/09942024
| Publication No. US/0030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. | APPLICANT: Fernandez-Salas, Ester | APPLICANT: Pernandez-Salas, Ester | APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANTON: Serotype A/E Toxins | TITLE OF INVENTION: Serotype A/E Toxins | TITLE OF INVENTION: Serotype A/E Toxins | CURRENT APPLICATION NUMBER: US/09/942,024 | CURRENT FILING DATE: 2001-08-28 | NUMBER OF SEQ ID NOS: 96 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 29 | LENORTH DATE | SEC ID NO 29 | LENORTH DATE | SEC ID NO 29 | SEQ ID NO 29 | LENORTH DATE | SEC ID NO 20 | LENORTH DATE | SEC I
                                PRIOR APPLICATION NUMBER: US 09/942,098
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: April 3, 2006, 15:26:53 Job time: 8.54839 secs
CURRENT FILING DATE: 2004-08-13
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Best Conservative
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ORGANISM: Homo sapiens
US-09-942-024-29
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; ORGANISM: Homo sapiens
US-10-917-844-28
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Query Match
100.0%; Score 39; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels
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INFORMATION FOR SEQ 1D NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
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6311, Ap
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Sequence 1, Appli
                                                                                                                                                   April 3, 2006, 15:16:44; Search time 2.12903 Seconds (without alignments) 310.660 Million cell updates/sec
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Sequence 10,
Sequence 11,
Sequence 18,
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Sequence 6
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Sequence
Sequence
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2 6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/6_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-743-894B-19
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US-09-962-360B-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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	743 - 894B-17 776 - 535A-9 776 - 535A-14 776 - 535A-14 776 - 535A-14 743 - 894B-51 743 - 894B-53 743 - 894B-64 743 - 894B-64 743 - 894B-64 743 - 894B-21 743 - 894B-21 848 - 748	BER: RMATION: 9-2065
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Sequence 13. Application US/09976535A

Factor No. 6504006

GENERAL INFORMATION:

APPLICANT: Shine, Nancy R.

APPLICANT: Saton, Linda J.

TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol)

TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum

FILE REFERENCE: PO10018

CURRENT APPLICATION NUMBER: US/09/976,535A

CURRENT APPLICATION NUMBER: US/09/976,535A

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

FINCE OF TAXABLE PATENTIAL OF TAXAB
Sequence 12, Application US/09976535A
Patent No. 6504006
GRNERAL INFORMATION:
APPLICANT: Shine, Nancy R.
APPLICANT: State, Crawford, Karen R.
APPLICANT: Eaton, Linda J.
TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol, TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum FILE REFERENCE: PO10018
CURRENT APPLICATION NUMBER: US/09/976,535A
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
FENCENTIAL OF 12
FENCENT
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100.0%; Score 39; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATURE:
CONTROLING ATTIFICIAL SEQUENCE
FEATURE:
COTHER INFORMATION: Synthetic peptide
NAME/KEY: misc feature
COTHER INFORMATION: Xaa represents D-Arg
NAME/KEY: misc feature
COCATION: (13)-..(13)
COCATION: (13)-..(13)
COCATION: (13)-..(13)
COCATION: (13)-..(13)
COCATION: Leu represents norleucine
US-09-976-535A-12
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) NAME/KEY: misc_feature

; LOCATION: (2)...(2)

; OTHER INFORMATION: Xaa represents D-Arg

US-09-976-535A-13
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EANORATK 12
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US-09-976-535A-13
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US-09-976-535A-2
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                                                                                                                                                                                                          Sequence 1, Application US/09976535A
Sequence 1, Application US/09976535A
Patent No. 65040ATON:
GENERAL INFORMATION:
APPLICANT: Shine, Nancy R.
APPLICANT: Eaton, Linda
TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
TITLE OF INVENTION WUMBER: US/09/976,535A
CURRENT PELLORIC DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 13
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Patent No. 6504006
GENERAL INFORMATION:
APPLICANT: Shine, Mancy R.
APPLICANT: Crawford, Karen R.
APPLICANT: Eaton, Linda J.
TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
FILE REFERENCE: P010018
CURRENT APPLICATION UNDER: US/09/976,535A
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
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OTHER INFORMATION: Leu represents norleucine
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OTHER INFORMATION: synthetic peptide
NAME/KEY: misc feature
LOCATION: (2)...(2)
OTHER INFORMATION: Xaa represents D-Arg
NAME/KEY: misc_feature
LOCATION: (13)...(13)...(13)
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5 EANORATK 12
                                     3 EANQRATK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: human
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US-09-976-535A-11
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US-09-976-535A-12
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US-08-743-894B-49
Sequence 49, Application US/08743894B
Sequence 49, A
                                                                                                       GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Varen A. Bostian
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STRET: USA NEWC.
STRET: USA NEWC.
STRET: GTT BETRICK
STATE: MARYLAND
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STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
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                        RESULT 8
US-08-743-894B-38
; Sequence 38, Application US/08743894B
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INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (301) 619-2065
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Best Local Similarity 100.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 EANORATK 15
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ZIP: 21702-5012
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Sequence 6, Application US/09976535A

Sequence 6, Application US/09976535A

Sequence 6, Application US/09976535A

GENERAL INFORMATION:
APPLICANT: Crawford, Karen R.
APPLICANT: Crawford, Karen R.
APPLICANT: Eaton, Linda J.

TITLE OF INVENTION: Batchity of Serotype A Neurotoxin from Clostridium botulinum FILE REFERENCE: P010018

CURRENT APPLICATION NUMBER: US/09/976,535A

CURRENT FILING DATE: 2001-10-12

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 6

LENGTH: 14
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OTHER INFORMATION: synthetic peptide
OTHER INFORMATION: synthetic peptide
LOCATION: (13) ... (13)
OTHER INFORMATION: Leu represents norleucine
NAME/KEY: misc_feature
LOCATION: (14) ... (14)
OTHER INFORMATION: Xaa represents D-Lys
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2, Application US/09976535A
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Best Local Similarity 100.۰
الا Si Conservative 8
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Best Local Similarity
Matches 8; Conserv
         Sequence 2, Applicati
Patent No. 6504006
GENERAL INFORMATION:
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Gaps ö

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Sequence 19, Application US/08743894B

Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin frontomes Properties of September S. 56
CORRESPONDENCE ADDRESS:
ADDRESSER: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
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; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-19
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                                                                                                                 Query Match
100.0%; Score 39; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels
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OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5565699ember 6, 1996
CLASSIFICATION 0435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-743-894B-24
Sequence 24, Application US/08743894B
; Patent No. 596569
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-7014
INFORMATION FOR SEC ID NO: 19:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid sequence
STRANDEDNESS: Single
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COUNTRY: USA
COUNTRY: USA
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100...
8, Conservative
                                    STRANDEDNESS: Single
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                                                      ; TOPOLOGY: Linear
US-08-743-894B-1
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US-08-743-894B-19
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Patent No. 5965699
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
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STREET: USA MRMC - 504 SCOtt Street
CITY: FORT DETRICK
STATE: MARYLAND
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CUREBLY APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 2955699ember 6, 1996
CLIASSIFICATION SATS:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
RESISTRATION NUMBER:
FILING DATE:
TELECOMMUNICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION 1000 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 anino acids
TYPE: amino acid sequence
TOPOLOGY: Linear
TOTOLOGY: Linear
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5565699ember 6, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER:
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NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-2065
TELEFAX: (301) 619-7014
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
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Best Local Similarity luv...
8; Conservative
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Sequence 36, Application US/08743894B
SEQUENCE 31 Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fro NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSES: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STREET: MARYLAND
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No. 5965699ember 6, 1996
          CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER:
APTICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFOXE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
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TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EANORATK 8
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ZIP: 21702-5012
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TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
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                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSE:
ADDRESSES:
ADDRESSES: MCMR.-JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER: Apple Macintosh 7.0
SOFWHYER: PROPPE Floppy disk
COMPUTER: PAPPE Floppy disk
COMPUTER: Macintosh 7.0
SOFWHYER: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6,1996
CLASSIPICATION NUMBER: 34,616
FILING DATE: ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 319,194
ITELEPHONE: (301) 619-2065
TELEFAX: (301) 619-2065
TELEFAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa represents norleucine US-08-743-894B-24
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Best Local Similarity 100.0%;
Marches 8; Conservative 0
  James J. Schmidt
Karen A. Bostian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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US-08-743-894B-28
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RESULT 15
19-743-791
19-804-737
19-804-743-79
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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                    ||||||||||
8 EANQRATK 15
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Search completed: April 3, 2006, 15:18:01 Job time : 3.12903 secs

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US-09-942-024-2
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Matches
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Sequence 12, Appli
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                                                                                                                                     April 3, 2006, 15:21:47; Search time 194.371 Seconds (without alignments) 442.828 Million cell updates/sec
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                                                                                                                                                                                                                                                            1048
1 MAEDADMRNELEEMQRRADQ.....SNKTRIDEANQRATKMLGSG 206
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-261-161-5

US-10-261-161-109

US-10-917-844-12

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US-10-131-844-14

US-10-723-860-1223

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US-10-723-860-1223

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US-10-723-860-123

US-10-723-861-14

US-10-942-098-16

US-10-917-844-14

US-10-917-844-16

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US-09-942-098-2
US-09-942-098-7
US-09-942-098-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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28 625.5 59.7 212 6 US-II-097-143-20133 Sequence 20133, A 618.5 59.0 212 3 US-09-94-024-13 Sequence 13, Appl 30 618.5 59.0 212 3 US-09-942-031 Sequence 13, Appl 1618.5 59.0 212 4 US-10-261-161-6 Sequence 6, Appl 32 618.5 59.0 212 5 US-10-261-161-6 Sequence 6, Appl 33 613.5 58.5 211 5 US-10-917-844-13 Sequence 13, Appl 34 609.5 58.2 211 5 US-10-917-844-13 Sequence 13, Appl 35 609.5 58.2 213 3 US-09-922-300-1718 Sequence 17.18, Appl 36 57.2 54.6 116 3 US-09-922-300-1718 Sequence 11, Appl 36 57.2 54.6 116 5 US-10-917-844-113 Sequence 11, Appl 40 572 54.6 116 4 US-10-917-844-112 Sequence 12, Appl 41 568 54.2 114 5 US-10-917-844-112 Sequence 12, Appl 44 403 38.5 86 4 US-10-705-857-1 Sequence 11, Appl 44 391.5 37.4 82 4 US-10-705-857-1 Sequence 1, Appl 45 11.5 37.4 82 4 US-10-705-857-1 Sequence 1, Appl 45 11.5 37.4 82 4 US-10-705-857-1 Sequence 1, Appl 45 11.5 37.4 82 4 US-10-705-857-1 Sequence 1, Appl 45 11.5 37.4 82 4 US-10-705-857-1 Sequence 1, Appl 45 11.5 37.4 82 4 US-10-705-857-1
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Sequence 2, Application US/09942024

Sequence 2, Application Wo. US2003014365011

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: APPLICANT: Permandez-Salas, Ester
APPLICANT: APPLICANT: Per Protease Assays For Botulinum
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT APPLICATION NUMBER: US/09/942,024
SUFFRENT APPLICATION NUMBER: US/09/942,024
SOFTWARER FILING DAME: 201-08-28
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.2e-85;
tive 0; Mismatches 0;
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; Publication No. US20030143650A1
; GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: ApplicANT:
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TYPE: PRT
ORGANISM: Homo sapiens
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61 EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
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Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
TITLE OF INVENTION: Tere Protease Assays For Clostridial
TITLE OF INVENTION: Tere Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Fernander-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REPERENCE: P-AR 4802.
CURRENT APPLICATION UNBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1048; DB 3;
; Pred. No. 1.2e-85;
0; Mismatches 0;
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100.0%; Pred. No. 1.2e-85;
ive 0; Mismatches 0;
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                                                                                                                         ; Sequence 2, Application US/09942098; Publication No. US20030143651A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 206; Conservative
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Matches 206; Conservative
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US-09-942-098-2
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US-09-942-098-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 BEGMDQINKDMKEAEKNLTDLGKPCGLCVCPCNKLKSSDAYKKAMGNNQDGVVASQPARV 120
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| Sequence 12, Application US/09942024
| Publication No. US20030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E.
| APPLICANT: Steward, Lance E.
| APPLICANT: Steward, Kel Roger
| TITLE OF INVENTION: Fret Protease Assays For Botulinum
| TITLE OF INVENTION: Serotype A/E Toxins
| FILE REFERENCE: P-AR 4803
| CURRENT PPLICATION NUMBER: US/09/942,024
| CURRENT FILING DATE: 2001-08-28
| NUMBER OF SEQ ID NOS: 96
| SOFFWARE: PRETENCE OF Windows Version 4.0
TITLE OF INVENTION: Fret Protease Assays For Botulinum TITLE OF INVENTION: Serotype A/E Toxins FILE REFERENCE: P-AK 4803 CURRENT APPLICATION NUMBER: US/09/942,024 CURRENT FILING DATE: 2001-08-28 NUMBER OF SEQ ID NOS: 96 COFTWARE: PASSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1048; DB 3; Best Local Similarity 100.0%; Pred. No. 1.2e-85; Matches 206; Conservative 0; Mismatches 0;
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; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12
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Best Local Similarity
Matches 206; Conserv
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ORGANISM: Rattus sp.

US-09-942-024-7
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; ORGANISM: Homo sapiens
US-10-261-161-4
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LENGTH: 206
TYPE: PRT
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Sequence 4, Application US/10261161

Sequence 7, Application No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT APPLICATION NUMBER: US/202-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
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publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 206; Conservative
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ORGANISM: Mus musculus
US-09-942-098-12
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LENGTH: 206
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Sequence 5, Application US/10261161

Sequence 5, Application US/10261161

Publication No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Tox:

TITLE OF INVENTION: Transfer (SCI)

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID DATE: 2002-09-27

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0;
Query Match
100.0%; Score 1048; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0;
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; ORGANISM: Mus musculus
US-10-261-161-5
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RESULT 11
US-10-917-844-12
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Publication No. US20050100973A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Marcella A.

APPLICANT: Acki, Kei R.

TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay

TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity

TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity

CURRENT APPLICATION NUMBER: US/10/917,844

CURRENT PILING DATE: 2004-08-13

PRIOR APPLICATION NUMBER: US 09/942,098

NUMBER OF SEQ ID NOS: 113

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 206
APPLICANT: Steward, Lance E.
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT PILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.2e-85;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 206; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Rattus sp.
US-10-261-161-109
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; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: AOKL, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT PEPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For Botulinum Neurotoxin Protease Activity
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                                                                                                                                                                                                                                                                               Sequence 12, Application US/10917844

Publication No. US20050100973A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Glimore, Marcella A.
APPLICANT: Glimore, Marcella A.
TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activi
TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activi
TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activi
CURRENT PRILICATION NUMBER: US/10/917,844

CURRENT PILING DATE: 2004-08-13
PRIOR PILING DATE: 2004-08-13
PRIOR PILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 113
SEQ ID NOS: 113
SEQ ID NOS: 113
FENERAL PRINCED FOR WINDOWS VERSION 4.0
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100.0%; Pred. No. 1.2e-85;
iive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH: 206
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                                                                  181 IMEKADSNKTRIDEANQRATKMLGSG 206
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ORGANISM: Artificial Sequence
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Matches 206; Conservative
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ORGANISM: Mus musculus
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LENGTH: 206
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                                                                                 Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%; Score 1004; DB 4; Length 206; 95.6%; Pred. No. 1e-81;
                                                                                                                                     Indels
                                                                           100.0%; Score 1048; DB 5;
100.0%; Pred. No. 1.2e-85;
tive 0; Mismatches 0;
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OTHER INFORMATION: synthetic construct
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Best Local Similarity 95.6'
Matches 197; Conservative
                                                                                                           Best Local Similarity 100.
Matches 206; Conservative
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US-10-318-417-3
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US-10-723-860-1223
              ; CIHEK INFORM
US-10-917-844-90
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                                                                                       Query Match
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Sequence 5012, Application US/10756149
| Sequence 5012, Application US/10756149
| Publication No. US20050181375A1
| GENERAL INFORMATION:
| APPLICANT: Allorik, Albert
| TITLE OF INVENTION: METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER | TITLE OF TOWENTY PAPLICATION NUMBER: US/10/756,149
| CURRENT APPLICATION NUMBER: US/10/756,149
| CURRENT PILING DATE: 2004-01-12 | SOGTWARE: PatentIn version 3.2 | SOGT
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION WUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
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95.8%; Score 1004; DB 5; Length 206;
Best Local Similarity 95.6%; Pred. No. 1e-81;
Matches 197; Conservative 5; Mismatches 4; Indels
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Pred. No. 1e-81;
5; Mismatches
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1223
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Matches 197; Conservative
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, ORGANISM: Homo Sapiens
US-10-756-149-5012
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US-10-723-860-1223
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181 IMEKADSNKTRIDEANQRATKMLGSG 206

Search completed: April 3, 2006, 15:26:52 Job time : 194.371 secs

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Sequence 4, Appli
Sequence 4, Appli
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Sequence 7, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 36, Appli
Sequence 21, Appli
Sequence 40, Appli
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Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
                                                                                                      April 3, 2006, 15:23:07; Search time 26.5806 Seconds (without alignments) 235.925 Million cell updates/sec
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1: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

6: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.7
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US-10-948-097-2
US-10-948-097-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Appl	Appl	Appl	Appl	28248, A	Appl	Appl	Appl	Appl	Appl	Appl	App	Apr								
29,	30,	44,	87,	2824	42,	42,	17,	20,	25,	54,	185,	665,	663,	661,	662,	660,	664,	999		
Sequence	Sednence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	
6 US-10-980-346B-29	US-10-980-346B-30	US-10-980-346B-44	US-10-467-962B-87	US-11-096-568A-28248	US-10-947-071-42	US-10-948-097-42	US-10-530-171-17	US-11-069-834-50	US-11-069-834-52	US-11-069-834-54	US-11-072-175-185	US-10-995-561-665	US-10-995-561-663	US-10-995-561-661	US-10-995-561-662	US-10-995-561-660	US-10-995-561-664	US-10-995-561-666	US-11-124-367A-264	
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12.3	12.3	12.3	10.4	10.4	10.2	10.2	10.2	10.2	10.1	10.1	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	
129	129	129	109	108.5	107	107	106.5	106.5	105.5	105.5	105	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104.5	
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ALIGNMENTS

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                                                                       APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REPRESENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 206
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Publication No. US20060063221A1
GENERAL INPORMATION:
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Best Local Similarity 100.
Matches 206; Conservative
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US-10-947-071-1
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RESULT 2 US-10-947-071-2 Sequence 2, Application US/10947071 ; Publication No. US20060063221A1

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TYPE: PRT
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APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: POR Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION: POR Determining Clostridial Toxin Activity
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 2
LENGTH: 206
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Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Plucescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
TITLE REFERENCE: 66872-040
TITLE REFERENCE: 204-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 206
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; Pred. No. 6.4e-75;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 206; Conservative 0
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CRGANISM: Homo sapiens
US-10-948-097-1
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US-10-947-071-2
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APPLICANT: Eristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
FILE REFERENCE: 10001 NP
FILE REFERENCE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR APPLICATION NUMBER: 60/584,405
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 225
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                                                               121 VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180
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APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: AoKi, Kei Roger
TITLE OF INVENTION: Pluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REPRENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 225, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
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RESULT 8
US-10-947-071-6
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APPLICANT: Gilmore, Marcella
APPLICANT: Geward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanchanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FASESEQ for Mindows Version 4.0
                                                                                       Query Match
100.0%; Score 1048; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 203;
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Pred. No. 5.3e-66;
7; Mismatches 12;
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; Publication No. US20060063221A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.3%;
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Carassius auratus
                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-225
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US-10-948-097-4
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LENGTH: 206
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; Sequence 4, Application US/10948097

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61 EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VDEREGMAISGGFIRRVINDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180
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APPLICANT: Williams,
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: Por Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILLING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSEQ for Windows Version 4.0
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
TAPLICANT: Gilmore, Marcella
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Fluorescence Folarization Assays For
TITLE OF INVENTION: Gilmore, Marcella
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REPRENCE: 66472-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
NUMBER PRESENTED FOR WINDOWS VERSION 4.0
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95.1%; Pred. No. 6.8e-63;
tive 5; Mismatches 4; Indels
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Publication No. US20060063221A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 89.1%;
Best Local Similarity 89.3%;
Matches 184; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Carassius auratus
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Best Local Similarity 95.1
Matches 175; Conservative
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ORGANISM: Gallus gallus
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US-10-948-097-5
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US-10-947-071-3
 SEQ ID NO 5
LENGTH: 212
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VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180
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APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEG DID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                             APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Glamce, Marcella
APPLICANT: Glamce, Marcella
APPLICANT: Aci, Kei Roger
TILLE OF INVENTION: Fluorescence Polarization Assays For
TILLE OF INVENTION: Determining Clostridial Toxin Activity
TILLE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 249
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95.1%; Pred. No. 6.8e-63;
tive 5; Mismatches 4;
                                                                                                                                                                                                                                                      ; Sequence 6, Application US/10948097; Publication No. US20060063222A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.13
Matches 175; Conservative
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; ORGANISM: Gallue gallus
US-10-948-097-6
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j Sequence 5, Application US/10948097

publication No. US20060053222A1

j GENERAL INFORMATION:

j APPLICANT: Verhagen, Marc

j APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

j APPLICANT: St
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                                                                                                                                                                                                   Query Match 59.8%; Score 627; DB 6; Length 212; Best Local Similarity 61.8%; Pred. No. 4.36-42; Matches 126; Conservative 29; Mismatches 45; Indels
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LENGTH: 212
TYPE: PRT
ORGANISM: Strongylcentrotas purpuratus
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TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 MAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHWALDMGNEIDTQNRQIDRIMEKAD 186
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                                               APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Acki, Kei Roger
ITILE OF INVENTION: Lanthanide-Based Substrates and Methods
ITILE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.0%; Score 618.5; DB 6; Length 212; Best Local Similarity 62.9%; Pred. No. 2e-41; Matches 124; Conservative 29; Mismatches 43; Indels 1
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APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Plucrescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66972-040
CURRENT APPLICATION UNDERF: US/10/948,097
CURRENT PILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10948097 Publication No. US20060063222A1 GENERAL INFORMATION:
Application US/10947071
No. US20060063221A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 SNKTRIDEANQRATKML 203
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SNEARIAVANORAHOLL 211
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Best Local Similarity 62.9%
Matches 124; Conservative
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ORGANISM: Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila sp. US-10-947-071-3
  Sequence 3, Applicati
Publication No. US200
GENERAL INFORMATION:
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Sequence 11, Application US/11195098

Publication No. US20050287622A1

GENERAL INFORMATION:

APPLICANT: Schmidt, James J.

APPLICANT: Stafford, Robert G.

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid);

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid);

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid);

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid);

FILE REPERBNCE: 003/224/SAP

CURRENT APPLICATION NUMBER: US/10/802,574

PRIOR FILING DATE: 2006-08-02

PRIOR FILING DATE: 2000-09-25

PRIOR PILING DATE: 2000-09-25

PRIOR PILING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Apple Macintosh Microsoft Word 6.0

SEQ ID NO 11.

TENGTON: 12
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APPLICANT: Stafford, Robert G.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi TITLE OF INVENTION: Heigh Throughput Assays for the Proteolytic Activities of Clostridi TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/11/195,098
PRIOR APPLICATION NUMBER: US/10/802,574
PRIOR APPLICATION NUMBER: US/10/802,574
PRIOR APPLICATION NUMBER: 09/962,360
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68 NKDMKEAEKNIJDLGKFCGLCVCPCNKLKSSDAYKKAWGNNODG-VVASQPARVVDEREQ 126
                                                                                                               61
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; Sequence 12, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
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195 SNEARIAVANQRAHQLL 211
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Search completed: April 3, 2006, 15:27:30 Job time : 27.5806 secs

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61 BEGMDQINXDMKBABKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
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Best Local Similarity 100.0%; Score 1048; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-97;
Matches 206; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Appli
Sequence 10848, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 916, Appli
Sequence 916, Appli
Sequence 10929, A
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Sequence 1, Appli
Sequence 6311, Ap
Sequence 10671, A
Sequence 11, Appl
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Sequence 915, App
Sequence 11104, A
                                                                                                                        (without alignments)
310.660 Million cell updates/sec
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                                                                                                                                                                 US-09-942-098-2
1048
1 MAEDADMRNELEEMQRRADQ......SNKTRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                     April 3, 2006, 15:16:44 ; Search time 54.8226 Seconds
               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/laa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/f_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
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US-09-949-016-10671

US-09-949-016-10671

US-09-952-368-12

US-09-952-368-12

US-09-9513-999C-7906

US-09-513-999C-7906

US-09-513-999C-7906

US-09-013-999C-7906

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US-09-953-09-916-10929

US-09-538-092-916
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 901, App
Sequence 8135, Ap
Sequence 11, Appli
Sequence 17, App
Sequence 8, Appli
Sequence 6417, Ap
Sequence 6134, Ap
Sequence 6925, Ap
Sequence 3, Appli
Sequence 131, Ap
Sequence 134, Ap
Sequence 121, Ap
Sequence 121, Ap
Sequence 121, Ap
Sequence 125, Ap
Sequence 16972, Ap
Sequence 16972, Ap
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CITY: Balo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
FLING DATE:
CLASSIFICATION NUMBER: US/08/393,985
FLILIGO DATE:
CLASSIFICATION NUMBER: 38,615
REFERENCE/POCKET NUMBER: 8600-0152
REFERENCE/POCKET NUMBER: 8600-0152
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 analmo acids
TYPE: amalmo acids
TYPE: amalmo acids
TYPE: amalmo acids
TYPE: ACCURED ALCOME ACCURED 
US-09-538-092-901
US-09-949-016-8888
US-09-310-187A-11
US-09-530-092-917
US-09-530-092-917
US-09-949-016-6417
US-09-949-016-6134
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US-09-949-016-8134
US-09-949-016-9199
US-09-949-016-10872
US-09-538-092-1321
US-09-538-092-1321
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Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: SCHOOLER, Richard H.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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FACEUL NO. 1001233.

FARENLE NO. 1001233.

FARENLE NO. 100123.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT PILING DATE: 2000-04-14

FRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10671

LENGTH: 219
                                                                                                                                                            SERVERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-10

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 6311
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100.0%; Pred. No. 2.4e-97;
ive 0; Mismatches 0;
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                                                                                                                 Sequence 6311, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 206; Conservative
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US-09-949-016-6311
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US-09-949-016-10671
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                                                                       RESULT 3
US-09-949-016-6311
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ORGANISM:
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                                                                               61 EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
                                                   VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180
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                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: DEUTOTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 425E Executive Square, Suite 1400
CITY: La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 1048; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.4e-97;
Matches 206; Conservative 0; Mismatches 0;
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                                                                                                                                                  181 IMEKADSNKTRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.,
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/00500
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08819286
Patent No. 6169074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
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sequence 10399, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

PILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF WINDOWS Version 4.0

SEQ ID NO 10399

LENGTH: 158
                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic peptide chosen such that it is cleaved by BONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 GFIRRVŢNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTR 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-09-962-360B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.9%; Score 512; DB 2; 53.6%; Pred. No. 1.1e-43; tive 22; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 572; DB 2;
Pred. No. 6.8e-50;
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.6%;
99.1%;
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
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NAME/KEY: misc_feature
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US-09-949-016-10399
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Best Local Simi
Matches 104;
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APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION WUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
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                                                                                                                                                                                                                                         121 VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHWALDMGNEIDTQNRQIDR 180
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                                                                                                                                                   14 MAEDADMRNELBEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
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                                     Length 219;
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55.2%; Score 578; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.7e-50;
Matches 114; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1
OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
                                   Score 1048; DB 2;
Pred. No. 2.6e-97;
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    194 IMEKADSNKTRIDEANQRATKMLGSG 219
                                                                                                                                                                                                                                                                                                                                                                                                 181 IMEKADSNKTRIDEANORATKMLGSG 206
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, Sequence 12, Application US/09962360B

; Patent No. 6762280

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09962360B
Patent No. 6762280
GENERAL INFORMATION:
                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial sequence
                                   Query Match
Best Local Similarity 100.0
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMAT
US-09-962-360B-11
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1 MAEDADMRNELBEMORRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
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43.0%; Score 451; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 8.5e-38;
Matches 90; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20005-334
ZIP: 20005-334
COMPUTER READABLE FORM:
BEDIUM TYRE: Ploppy disk
COMPUTER: IBM PC COMPACIBLE
COMPUTER: PARCENTINE RELEASE #1.0, Version #1.30
SOFTWARE: PRECEDIN NECLEGE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: WCT/GB95/01279
FILING DATE: PCT/GB95/01279
FILING DATE: PCT/GB95/01279
FILING DATE: PCT/GB95/01279
FILING DATE: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 1581.0120001
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2643
TREEPHONE: 202-371-2543
TREEPHONE: 202-371-2543
TREEPHONE: 202-371-2543
TREEPHONE: 202-371-2543
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                                                                                                                                                                      LOCATION: 72
OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Banne, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Golds
                                            NAME/KEY: UNSURE
LOCATION: 71
OTHER INFORMATION: Xaa=Met or Arg
                                                                                                                                                                                                                     FEATURE:

NAME/KEY: UNSURE

LOCATION: 92

OTHER INFORMATION: Xaa=Gly or Val
US-09-513-999C-7907
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
ORGANISM: Homo sapiens
                                                                                                                    FEATURE:
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-760-001-10
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                                                                                                                         US-09-51-999C-7906

US-09-513-999C-7906

Sequence 7966, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dundae Milne Edwards, J.B.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT.PM

SEQ ID NO 7906

LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7907, Application US/09513999C
; Sequence 7907, Application US/09513999C
; Retent No. 6783961
; GENERAL INFORMATION:
    APPLICANT: Dummes Milne Edwards, J.B.
; APPLICANT: Duclett, A.
; APPLICANT: Duclett, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT SERVENCE: 59.US2.REG
    CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-24
; PRIOR PILING DATE: 1999-02-26
; NUMBER: OF SEQ ID NOS: 36681
; SOFTWARE: PATENT.PM
; SEQ ID NO 7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: UNSURE
LOCATION: 72
OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa=Met or Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Xaa=Gly or Val
US-09-513-999C-7906
192 IDEANQRATKMLGS 205
                                                  145 iDIANARAKKLIDS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-09-534-572-10
                               US-09-534-572-10
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                                                                                                                 137 VTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN
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                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
    APPLICANT: Shone, Clifford C.
    APPLICANT: Hallis, Bassam
    APPLICANT: James, Benjamin A. F.
    APPLICANT: Oulnn, Conrad P.
    TITLE OF INVENTION: TOXIN ASSAY
    NUMBER OF SEQUENCES: 11
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
    STREET: 1100 New York Ave., N.W., Suite 600
    CONTACT. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 70;
                               33.7%; Score 353; DB 1; Length 70; 100.0%; Pred. No. 3.4e-28; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.7%; Score 353; DB 2; 1
100.0%; Pred. No. 3.4e-28;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: RIDAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTOWNEY ASSISTANCE OF THE SEGRET AND RECISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 158
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371.2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 70; Conservative
                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-09-015-960-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 ORATKMLGSG 206
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                                                        Best Local Similarity
Matches 70; Conserv
US-08-760-001-10
                                       Query Match
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137 VINDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.7%; Score 353; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.4e-28;
Matches 70; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
FRIING APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bemond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-513-999C-4845
'S-Sequence 4845, Application US/09513999C
'Petent No. 6783961
Sequence 10, Application US/09534572;
Patent No. 6337386;
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: James, Benjamin A. F.
TITLE OF INVENTION: CORTAG P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: Herewith CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QRATKMLGSG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAEDADMRNELEERQRRADQLADESLESTRRMLQLVEESKDAGIRTLVWLDEQGEQLERI
        TITLE OF INTEGRATION Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REPERENCE: 59.022.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR PAPLICATION NUMBER: US 60/122,487
PRIOR PAPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SSC ID NO 4845
LENGTH: 64
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                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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29.6%; Score 310; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.2e-24;
Matches 64; Conservative 0; Mismatches 0; Indels
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Patent No. 6784341
GENERAL INFORMATION:
APPLICANT: Johal, Gurmukh S.
APPLICANT: Multani, Dilbag
TITLE OF INVENTION: Defense-Related Signaling Genes and
TITLE OF INVENTION: Methods of Use
FILE REPERENCE: 35718/237947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-621-976-7614

Sequence 7614, Application US/09621976

Sequence 7614, Application US/09621976

GENERAL INFORMATION:

APPLICANT: Under Mine Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Jobert, S.

TITE REFERENCE: GENSET.054PR2

FILE REFERENCE: GENSET.054PR2

CURRENT FILIG DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NOS: 19335

SEQ ID NO 7614

LENGTH: 68
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CURRENT FILING DATE: 2001-09-14
PRICA APPLICATION NUMBER: 60/232,538
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 9
Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Homo sapiens
US-09-621-976-7614
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US-09-952-689-9
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Best Local S:
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71 MKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQ----DGVVASQ---PARVVDE 123
                                                                                                                                                                                                                                                                                                                                                                   202 LEKREKLGINSAPRGQSRTREPLPESADAYQRV--EMEKAKQDDGLSDLSDLGELKNMA 259
                                                                                                                                                                                                                                             11 LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKD 70
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                          44;
                                                                                                                                                      Query Match

21.9%; Score 230; DB 2; Length 300;
Best Local Similarity 27.3%; Pred. No. 5.3e-15;
Matches 60; Conservative 45; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 LDMGNEIDTONROIDRIMEKADSNKTRIDEANORATKMLG 204
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 300
                                                                                           ; ORGANISM: Arabidopsis
US-09-952-689-9
                                                                        TYPE: PRT
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Search completed: April 3, 2006, 15:18:00 Job time : 55.8226 secs

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Sequence 6, Appl:
                                                                                              April 3, 2006, 15:23:07; Search time 2.19155 Seconds (without alignments) 235.925 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37,
Sequence 33,
Sequence 33,
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Sequence 35,
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1: /SIDSS/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

2: /SIDSS/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

6: /SIDSS/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptcdata/1/pubpaa/US11_NEW_PUB.pep:*

8: /SIDSS/ptcdata/1/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                                                           180808 seqs, 30441898 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                   US-09-942-098-2_COPY_187_203
83
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence 225, Sequence 20, P Sequence 41, Sequence 36, Sequence 40, Sequence 36, Sequence 40, Sequence 41, Sequence 4, Sequence 11 Sequence 1, Sequence 2, Sequence Sequence Sequence US-10-980-346B-6
US-10-980-346B-37
US-10-947-071-33
US-10-947-071-35
US-10-947-071-35
US-10-947-071-36
US-10-947-071-40
US-10-947-071-40
US-10-947-071-41
US-10-948-097-40
US-10-948-097-41
US-10-948-097-41
US-10-948-097-41
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US-10-948-097-41
US-10-948-097-2
US-10-947-071-1
US-10-948-097-2
US-10-947-071-2
US-10-947-071-2
US-10-948-097-2
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US-10-948-097-20
US-10-948-097-21 100.0 100.0 100.0 000

Sequence Sequence 3 Sequence

Sequence

605 605 605 605 605 605	Sequence 58, Appl Sequence 62, Appl Sequence 62, Appl Sequence 58, Appl Sequence 58, Appl Sequence 38, Appl Sequence 38, Appl Sequence 51, Appl Sequence 51, Appl Sequence 56, Appl	ds for Detection and Differentiation
σοσοσοσοσ	17 6 US-10-947-071-54 17 6 US-10-947-071-58 17 6 US-10-948-097-54 17 6 US-10-948-097-58 17 6 US-10-948-097-58 17 6 US-10-948-097-51 17 6 US-10-948-097-51 17 6 US-10-947-071-51 17 6 US-10-947-071-51 17 6 US-10-947-071-51 17 6 US-10-947-071-51	ULT 1 10-980-346B-6 quence 6, Application US/10980346B ublication No. US20060024763A1 ENERAL INFORMATION: ENPELICANT: Los Alamos National Laboratory APPLICANT: Los Alamos National Laboratory APPLICANT: Schmidt, Jurgen G., et al. TITLE OF INVENTION: of Botulinum Neurotoxins FITLE OP INVENTION: of Botulinum Neurotoxins CURRENT APPLICATION NUMBER: US/10/980,346B CURRENT FILING DATE: 2004-11-03 NUMBER OF SEQ ID NOS: 55 NOFFWARE PERFORMENT PLANCES APPLICATION NUMBER: 2004-11-03
79 95.2 79 95.2 79 95.2 79 95.2 79 95.2 79 95.2		SULT 1 -10-980.346B-6 Sequence 6, Application US/10980346B Sequence 6, Application US/10980346B SEQUENCE 100 NO. US20060024763A1 GENERAL INFORMATION: APPLICANT: Los Alamos National Labo APPLICANT: Schmidt, Jurgen G., et TITLE OF INVENTION: Mass Spectromet TITLE OF INVENTION: of Botulinum NFILE REPRENCE: S-102,313 CURRENT APPLICATION NUMBER: US/10/9 CURRENT FILING DATE: 2004-11-03 NUMBER OF SEQ ID NOS: 55 CONTWAND: DatantIn version 3.2
2 2 2 2 2 2 2 2 3 3 3 3 3 3 4 3 3 4 3 4	8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT 1 US-10-980-346B-6 ; Sequence 6, Ap. ; Publication NO ; GENERAL INFORM APPLICANT: LO ; TITLE OF INVE TITLE REPERENC ; CURRENT APPLI ; CURRENT APPLI ; CURRENT PILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN

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Sequence 37, Application US/10980346B

Sequence 37, Application US/10980346B

Publication No. US20060024763A1

Sembral INFORMATION:
APPLICANT: Los Alamos National Laboratory
APPLICANT: Schmidt, Jurgen G. 1 al.
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
TITLE OF INVENTION: of Botulinum Neurotoxins
FILE REFERENCE: S.102,313
CURRENT RELING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 55
SOFTWARE PATENTIAL OF SEQ ID NOS: 55
SOFTWARE PATENTIAL OF SEQ ID NOS: 55
SEQ ID NO 37
LENGTH: 17
                                                                                                    ; OTHER INFORMATION: Synthetic peptide chosen such that it is cleaved by a Botulinum; OTHER INFORMATION: Neurotoxin (BONT)
US-10-980-346B-6
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                                                           TYPE: PRT
ORGANISM: Artificial Sequence
PatentIn version 3.2
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Best Local Similarity 100...
Local 17; Conservative
  SOFTWARE: E
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; Sequence 35, Application US/10947071
; Publication No. US2006006321A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: Lanthanide-Based Substrates
; TITLE OF INVENTION: Lanthanid
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APPLICANT: Verhagen, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Greward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOPTWARE: FastSEQ for Windows Version 4.0
LEMOTH. 19
                                                                 Length 17;
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100.0%; Pred. No. 8.6e-09;
tive 0; Mismatches 0;
                                                             Query Match 100.0%; Score 83; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
....hes 17; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-948-097-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-947-071-35
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US-10-948-097-33
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TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
OTHER INFORMATION: Neurotoxin (BoNT)
FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (1)...(17)
OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37
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APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger,
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REPERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 17
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Sequence 33, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Williams, Dudley J.

APPLICANT: Gilmore, Marcella

APPLICANT: Acki, Kei Roger

ITLE OF INVENTION: Pluorescence Polarization Assays For

ITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REFERENCE: 6687-040

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FASTESQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 17
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Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
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100.0%; Score 83; DB 6; I
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0;
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; Sequence 33, Application US/10947071
; Sequence 33, Application No. US20060063221A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gaps
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Sequence 36, Application US/10948097

Publication No. US2006006322A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marcella

APPLICANT: Steward, Lance

APPLICANT: Stew
                         APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 204-09-21
NUMBER OF SEG ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20060063222A1

GENERAL INFORMATION:
APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Glimore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Acki, Kel Roger
TITLE OF INVENTION: Pluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
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                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ; ORGANISM: Carassius auratus US-10-947-071-41
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
Steward, Lance
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LENGTH: 33
   APPLICANT:
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Sequence 40, Application US/10947071

Sequence 40, Application US/10947071

Publication No. US20060063221A1

GENERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 40

LENGTH.
                                                                                                                                                                                                                                                                                                                APPLICANT: Standard, Lance, APPLICANT: Standard, Lance, APPLICANT: Steward, Lance, APPLICANT: Steward, Lance, APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: Lor Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICANTON NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 33
TYPE: RRT
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                                                                                                                                           Sequence 36, Application US/10947071
Publication No. US20060053221A1
GENERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 SNKTRIDEANQRATKML 30
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US-10-947-071-36
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CURRENT APPLICATION NUMBER: US/10/948,097 CURRENT FILING DATE: 2004-09-22 NUMBER OF SEQ ID NOS: 96

APPLICANT: Williams, Dudley J. APPLICANT: Gilmore, Marcella

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OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT
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Sequence 4, Application WS/10947071

Publication No. US2060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Verhagen, Marc

APPLICANT: Verhagen, Marc

APPLICANT: OF INVENTION: Lanchanide-Based Substrates and Methods

TITLE OF INVENTION: Lanchanide-Based Substrates and Activity

FILE REPRESENCE: 66872-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT PILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 203
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Sequence 4, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Gilmore, Marcella

APPLICANT: Gilmore, Marcella

APPLICANT: Gilmore, Marcella

APPLICANT: Acki, Kei Roger

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Determining Clostridial Toxin Activity

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REPRENCE: 66872-040

CURRENT APPLICATION UNMBER: 2004-09-22

CURRENT FILING DATE: 2004-09-22

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

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LENGTH: 203

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                                                                                                                                                                         100.0%; Score 83; DB 7; Length 116; 100.0%; Pred. No. 7.7e-08; ive 0; Mismatches 0; Indels
                                                    NAME/KEY: misc_feature
LOCATION: 1
. TOTATION: 1
. OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-11-195-098-11
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity
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Sequence 11, Application US/11195098

Publication No. US20050287622A1

GENERAL INFORMATION:

APPLICANT: Schmidt, James J.

APPLICANT: Schmidt, James J.

APPLICANT: Schmidt, James J.

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid

TITLE OF INVENTION: MUMBER: US/11/195,098

CURRENT APPLICATION WUMBER: US/10/802,574

PRIOR FILING DATE: 2004-03-17

PRIOR FILING DATE: 2004-03-17

PRIOR FILING DATE: 2000-09-25

PRIOR PILING DATE: 2000-09-25

PRIOR PILING DATE: 2001-09-25

PRIOR PILING DATE: 2001-09-25

PRIOR PILING DATE: 2001-09-25
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JAPPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
JAPPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Gteward, Lance
APPLICANT: Aoki, Kei Roger
TITEE OF INVENTION: Fluorescence Polarization Assays For
TITEE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
JENGTH: 33
TYPE: PRT
                                                                                                                                                                                   Length 33;
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100.0%; Score 83; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                   Score 83; DB 6; 1
Pred. No. 1.8e-08;
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100.0%; Score 83; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 17; Conservative 0; Mismatches
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SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
EENGTH: 116
     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40 LENGTH: 33
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; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    1 SNKTRIDEANORATKML 17
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ORGANISM: Artificial sequence
FEATURE:
                                                                                                        ; ORGANISM: Carassius auratus
US-10-948-097-40
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US-10-948-097-41
                                                                                TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-942-098-30
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52, Sequence 58, Sequence 30, Sequence 32, Sequence 54, Sequence 54, Sequence 54, Sequence 32,
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Sequence 90,
Sequence 90,
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Sequence 37,
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Sequence 33,
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Sequence 55,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-00-011-58-30

US-10-011-58-2

US-10-261-161-68

US-10-917-844-30

US-09-942-098-32

US-09-942-024-32

US-09-942-024-89

US-09-942-024-89

US-09-942-024-89

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                                                                                                                                                                                                                                         1867569 seqs, 417829326 residues
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83
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Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
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Maximum DB seq length: 200000000
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Sequence 30, Application US/09942098
Sequence 30, Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-A 4802
CURRENT APPLICANT: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOUTHAR: PastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 83; DB 3; Length 17; 100.0%; Pred. No. 3.4e-07; tive 0; Mismatches 0; Indels
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Publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Sercityee A/E Toxine

TITLE OF INVENTION: Sercityee A/E Toxine

FILE REPERENCE: P-AR 4803

CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT PILING DATE: 2010-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30
US-10-917-844-37

US-10-917-844-38

US-10-705-857-4

US-10-917-844-112

US-09-962-360B-11

US-09-942-054-14

US-09-942-058-14

US-10-261-161-7

US-10-261-161-7

US-09-942-024-12

US-09-942-024-12

US-09-942-024-12

US-09-942-024-12

US-09-942-038-2

US-09-942-098-7

US-09-942-098-7

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US-09-942-098-7

US-09-942-08-12

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      TYPE: PRT
ORGANISM: Homo sapiens
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WESTOL 3

WESTOL 3

WESTOL 1588-2

SEQUENCE 2, Application US/10011588

PUBLICANT: US20020168727A1

GENERAL INFORMATION:

APPLICANT: Smith, Leonard

APPLICANT: Jennen, Melody

TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM

TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM

TITLE OF INVENTION: RECOMBINANT LIGHT CHAIN FUSION PROTEINS FOR USE IN

TITLE OF INVENTION: RESPREAD AND CLINICAL THERAPY

FILE REPERENCE: A34796 667252.013

CURRENT APPLICATION NUMBER: US/10/011,588

CURRENT APPLICATION NUMBER: 00/20/31.086

PRIOR FILING DATE: 2001-07-20

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 47

WUMBER OF SEQ ID NOS: 47

WANDER OF LENGTH APPLICATION NUMBER: 60/311,966

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 47

WANDER OF LENGTH: 17
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Bublication No. US20040072270A1

GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 17
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Query Match
100.0%; Score 83; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2
                                                                                                                       1 SNKTRIDEANORATKML 17
                                                                                                                                              1 SNKTRIDEANQRATKML 17
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; ORGANISM: Homo sapiens
US-10-261-161-52
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| Sequence 30, Application US/10917844
| Publication No. US20050100973A1
| Publication No. US20050100973A1
| Publication No. US20050100973A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. | APPLICANT: Gilmore, Marcella A. |
| TILLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay | TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity | TILLE DEFERRENCE: 66872-044 | CURRENT APPLICATION NUMBER: US/10/917,844 | CURRENT FILING DATE: 2004-08-13 | PRIOR PILING DATE: 2004-08-28 | NUMBER OF SEQ ID NOS: 113 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 30 | LENGTH: 17
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; Publication No. US20040072270A1
; Publication No. US20040072270A1
; GENERAL INPORMATION:
    APPLICANT: Pernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Acki, Kei Roger
; TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxii;
; FILE REPERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT PILLING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 68
; ERNGTH: 17
Query Match 100.0%; Score 83; DB 4; Length 17; Best Local Similarity 100.0%; Pred. No. 3.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: synthetic construct US-10-261-161-68
                                                                                                                                                 1 SNKTRIDEANQRATKML 17
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ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 18
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 17; Conservative
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US-10-917-844-32
                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-54
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
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| Sequence 32, Application US/09942098
| Publication No. US20030143651A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. |
| APPLICANT: Steward, Lance E. |
| APPLICANT: Permadez-Salas, Ester |
| APPLICANT: Aoki, Kei Roger |
| TITLE OF INVENTION: Fret Protease Assays For Clostridial |
| TITLE OF INVENTION: Toxins |
| TITLE OF INVENTION: Toxins |
| FILE REFERENCE: P-AR 4802 |
| CURRENT APPLICATION NUMBER: US/09/942,098 |
| CURRENT FILING DATE: 2001-08-28 |
| NUMBER OF SEQ ID NOS: 96 |
| SEQ ID NO 32 |
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           RESULT 7
US-09-942-024-32
is equence 32, Application US/09942024
j Publication No. US20030143650A1
igenstal information:
j APPLICANT: Steward, Lance E.
j APPLICANT: Rernandez-Salas, Ester
j TITLE OF INVENTION: Fret Protease Assays For Botulinum
j TITLE OF INVENTION: Fret Protease Assays For Botulinum
j TITLE OF INVENTION: Pret Protease Assays For Botulinum
j TITLE OF INVENTION: Serotype A/E Toxins
j CURRENT PLILIG DATE: 2001-08-28
i CURRENT FILING DATE: 2001-08-28
i NUMBER OF SEQ ID NOS: 96
j SEQ ID NOS: 96
j SEQ ID NO 32
i LENGTH: 18
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; Sequence 54, Application US/10261161
; Publication No. US20040072270A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNKTRIDEANORATKML 18
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Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Sequence 6, Application US/10705857;
Sequence 6, Application US/10705857;
Publication No. US20040147443A1
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF A COMBINATION OF COMPONENTS WITH AN INHIBITORY
TITLE OF INVENTION: SYNERGISTIC BFFECT ON CALCIUM CHANNELS TO PREVENT OR
TITLE OF INVENTION: TERAT WRINKLES AND FINE LINES
TITLE OF INVENTION: TERAT WRINKLES AND FINE LINES
TITLE OF INVENTION: TERAT WRINKLES AND FINE LINES
CURRENT APPLICATION WUMBER: 60/427, 575
CURRENT PILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
SPRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 19
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US-10-917-844-32
; Sequence 32, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Glimore, Marcella A.
; APPLICANT: Glimore, Marcella A.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR FILING DATE: 2004-08-13
; PRIOR FILING DATE: 2001-08-28
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Length 18;
                                                      0; Indela
     100.0%; Score 83; DB 4; 100.0%; Pred. No. 3.6e-07;
                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 18
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SNKTRIDEANORATKML 17
                                                                                                                                                               2 SNKTRIDEANORATKML 18
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity
                                                                                                                                                   NAME/KEY: AMIDATION LOCATION: (0)...(0)
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US-09-942-024-88
                                                                                                                                                                                                                    US-09-942-098-89
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NAME/KEY: MOD_RES
LOCATION: INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 2.1
COTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 89, Application US/09942098
; Bublication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas,
TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; TITLE OF INVENTION: Toxins
; TITLE OF INVENTION: Toxins
; TITLE OF LAPPLICATION WINDER: US/09/942,098
; CURRENT APPLICATION WINDER: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
LENGTH: 21
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Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                  Length 19;
                                                                                                                                                                                                                                                                                     Sequence 89, Application US/09942024
; Sequence 89, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
    APPLICANT: Steward, Lance E.
    APPLICANT: Fernandez-Salas, Ester
    APPLICANT: Fernandez-Salas, Ester
    TITLE OF INVENTION: Fret Protease Assays For Botulinum
    TITLE OF INVENTION: Serctype A/E Toxins
    FILE REFERENCE: Past 4803
; CURRENT FALING DATE: 2001-08-28
    NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
    LENGTH: 21
                                                                                                          Indels
                                                              Query Match
100.0%; Score 83; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0;
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OTHER INFORMATION: at the C-terminal
                                                                                                                                                          1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                      3 SNKTRIDEANORATKML 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SNKTRIDEANQRATKML 17
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
; OTHER INFORMATION: peptide US-10-705-857-6
                                                                                                                                                                                                                                                                  RESULT 12
US-09-942-024-89
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                                                                                                                                           LOCATION: 21 - OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 23 -
OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 83; DB 3; Length 23; 100.0%; Pred. No. 4.8e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 83; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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Sequence 88, Application US/09942024

; Publication No. US20030143650A1

; GAPLICANT: Steward, Lance E.

; APPLICANT: Steward, Lance E.

; APPLICANT: Perrandez-Salas, Ester

; APPLICANT: Porti, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum

; TITLE OF INVENTION: Fret Protease Assays For Botulinum

; TITLE OF INVENTION: Serotype A/E Toxins

; CURRENT APPLICATION NUMBER: US/09/942,024

; CURRENT FILING DATE: 2001-08-28

; NUMBER OF SEQ ID NOS: 96

; SEQ ID NO 88

; LENGTH: 23
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fornandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: I
OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: AMIDATION
LOCATION: (0)...(0)
CTHER INFORMATION: at the C-terminal
US-09-942-024-88
                                                                                                                                                                                                                                      LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNKTRIDEANORATKML 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SNKTRIDEANORATKML 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
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CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 88

LENGTH: 23

TYPE: PROFESTATION: Synthetic peptide

FRATURE:
ORCANISM: Artificial Sequence
FRATURE:
ORCANISM: Artificial Sequence
FRATURE:
ORCANISM: AND RES

LOCATION: 1

OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES

LOCATION: 23

OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION

COTHER INFORMATION: at the C-terminal

COTHER INFORMATION: at the C-terminal

US-09-942-098-88

Query Match

Best Local Similarity 100.0%; Pred. No. 4.8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: April 3, 2006, 15:26:52 Job time : 16.0403 secs

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Sequence 38, Sequence 3,

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Aren A. Bostian
TITLE OF INTENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fro
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSES: MARK—5 64 Scott Street
ADDLESSES: MACHOS MARK—5 66 Scott Street
ADDLESSES: MACHOS MARK—5 66 Scott Street
ADDLESSES: MACHOS MARK—5 64 Scott Street
ADDLESSES: MACHOS MACHOS MARK—5 64 Scott Street
ADDLESSES: MACHOS MACHO
Sequence 24, Sequence 28, Sequence 28, Sequence 31, Sequence 34, Sequence 44, Sequence 46, Sequence 46, Sequence 8, Sequence 8, Sequence 8, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 12,
                                                                                                                                                                                                                                                                      Sequence 35,
Sequence 47,
Sequence 48,
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100.0%; Pred. No. 5.1e-08;
tive 0; Mismatches 0; Indele
US-08-743-894B-24
US-08-743-894B-26
US-08-743-894B-31
US-08-743-894B-34
US-08-743-894B-34
US-08-743-894B-34
US-08-743-894B-34
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-21
US-08-743-894B-21
US-08-743-894B-35
US-08-743-894B-35
US-08-743-894B-35
US-08-743-894B-35
US-08-743-894B-38
US-08-743-894B-38
US-08-743-894B-38
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US-08-743-894B-38
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; Patent No. 5965699
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Sequence 37, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 13, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 32, Appli
Sequence 25, Appli
                                                                                                                                                    April 3, 2006, 15:16:44 ; Search time 4.52419 Seconds (without alignments) 310.660 Million cell updates/sec
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Sequence 2,
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                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1. /cgr2_6/ptodata/1/iaa/5_COMB.pep:*

2. /cgr2_6/ptodata/1/iaa/6_COMB.pep:*

3. /cgr2_6/ptodata/1/iaa/H_COMB.pep:*

4. /cgr2_6/ptodata/1/iaa/PeTUS_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/RE_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/RE_COMB.pep:*

6. /cgr2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-743-894B-37
US-08-819-286-9
US-08-819-286-4
US-08-78-72-10
US-09-534-572-10
US-09-534-572-10
US-09-949-1016-6311
US-08-39-985-18
US-08-39-985-18
US-08-39-985-18
US-08-39-985-18
US-08-34-894B-18
US-08-743-894B-39
US-08-743-894B-29
US-08-743-894B-29
US-08-743-894B-29
US-08-743-894B-29
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US-08-743-894B-2
US-08-743-894B-20
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                    572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                 US-09-942-098-2_COPY_187_203
83
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                              1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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1000.0
1000.0
1000.0
96.4
95.2
95.2
95.2
95.2
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Score

Result No.

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Gaps

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US-08-819-286-8
; Sequence 8, Application US/08819286
; Sequence 8, Application US/08819286
; Patent No. 6158074
; GENERAL INFORMATION:
    TITLE OF INVENTION: PERTIDE INHIBITORS OF
    TITLE OF INVENTION: PERTIDE INHIBITORS OF
    TITLE OF INVENTION: PERTIDE OF INVENTION BY NEURONAL CELLS
    NUMBER OF SEQUENCES: 29
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: fish & Richardson P.C.
    STREET: 4225 Executive Square, Suite 1400
    CITY: La Jolla
    STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 83; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Pc-Dos/MS-Dos
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION NUMBER: US/08/819,286
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTONNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 37,849
REGISTRATION NUMBER: 37,849
REGISTRATION NUMBER: 37,842
REFERENCE/DOCKET NUMBER: 37,842
REGISTRATION NUMBER: 37,843
REGI
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SNKTRIDEANORATKML 17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Taylor, Stacy L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-819-286-9
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                                                                                                                                    Sequence 37, Application US/08743894B

Sequence 37, Application US/08743894B

Patent No. 585589

GENERAL INFORMATION:
APPLICANT: Acreen & Schmidt
APPLICANT: Acreen & Boesian

TITLE OF INVENTION: Assay for the Protecolytic Activity of Serotype A Neurotoxin fr

NUMBER OF SEQUENCES:
ADDRESSE:
ADDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-743-894B-37
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US-08-819-286-9
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Gaps

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Shone, Clifford C.
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Sequence 4, Application US/08819286

Setent No. 6169074

GENERAL INFORMATION:
APPLICANT: MOITEL, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: PERTIDE INHIBITORS OF
TITLE OF INVENTION: DEBROYRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla
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                                                                                                                       Length 26;
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286 FILING DATE:
                                                                                                                     Query Match
100.0%; Score 83; DB 2; I
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/00500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLGGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                        1 SNKTRIDEANORATKML 17
                                                                                                                                                                                                                                   7 SNKTRIDEANQRATKML 23
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
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Best Local Similarity 100.0
Matches 17; Conservative
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                     US-08-819-286-8
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US-08-819-286-4
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Sequence 10, Application US/08760001 Patent No. 5962637 GENERAL INFORMATION:

US-08-760-001-10

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Patent No. 6043042

GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Contad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 83; DB 1; Length 70; 100.0%; Pred. No. 2.6e-07; tive 0; Mismatches 0; Indels
                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
Hallis, Bassam
James, Benjamin A. F.
Quinn, Conrad P.
VENTION: TOXIN ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 SNKTRIDEANQRATKML 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SNKTRIDEANORATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0
Matches 17; Conservative
 APPLICANT: Hallis, Bass:
APPLICANT: James, Benjar
APPLICANT: Quinn, Conrac
TITLE OF INVENTION: TOX.
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-10
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TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
  TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                     ; MOLECULE TYPE: peptide US-09-534-572-10
                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-393-985-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SUSPENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                       NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REPERENCY/DOCKET NUMBER: 1581.0120001
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09534572;
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A.F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OP SEQUENCES: 19
                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
                                                                                                                                                                                                                                                                       TELEFAX: 202-311-2543
TELEFAX: 202-311-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNKTRIDEANQRATKML 67
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-015-960-10
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APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OP INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridis TITLE OP INVENTION: Help Throughput Assays for the Proteolytic Activities of Clostridis TITLE OP INVENTION: Neurotoxins FILE REFERENCE: 003/224/SAP CURRENT APPLICATION NUMBER: 18,09/962,360B CURRENT PILING DATE: 2002-08-19 PRIOR APPLICATION NUMBER: US 60/235,050 PRIOR FILING DATE: 2001-09-25 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Apple Macintosh Microsoft Word 6.0 SEQ ID NO 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
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                                                                  Gaps
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Query Match
100.0%; Score 83; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
i LOCATION: 1
CTHEN INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-3608-13608-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                 US-09-962-360B-11; Sequence 11, Application US/09962360B; Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 SNKTRIDEANORATKML 112
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                                                                                                                           1 SNKTRIDEANORATKML 17
                                                                                                                                                                                 51 SNKTRIDEANORATKML 67
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ORGANISM: Artificial sequence
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1 SNKTRIDEANORATKML 17
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not relevant
                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Human
US-09-949-016-10671
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US-09-949-016-10671
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TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 83; DB 1; Length 206; ilarity 100.0%; Pred. No. 9.1e-07; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/POCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acide
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RIOR APPLICATION DATA:
PAPLICATION NUMBER: US 60/013,599

PILING DATE: 18-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842

REPERENCE/DOCKET NUMBER: 07349/00506

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08819286 Patent No. 6169074 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 17; Conserv
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; Sequence 6311, Application US/09949016
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFFWARE: PRESERQ FOR WINDOWS VERSION 4.0
SEQ ID NO 10671
LENGTH: 219
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Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 83; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0;
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Patent No. 6812339
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FEATURE
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Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Amen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES:
ADDRESSES: MCMR-JA Attn.John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Query Match 100.0%; Score 83; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 9.8e-07; Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: FORT DELALLS.
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6,1996
CLASSIFICATION NUMBER: US/08/743,894B
FILING DATE: NO. 5965699ember 6,1996
CLASSIFICATION NUMBER: 33
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 31,616
RELEPHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
FUNDER SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
FUNDER SEQUENCE CHARACTER SEQUENCE CHARACTERISTICS:
FUNDER SEQUENCE CHARACTER SEQUENCE CHARA
                                                                                                                                                                                                                   200 SNKTRIDEANORATKML 216
                                                                                                                                                1 SNKTRIDEANQRATKML 17
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TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNKTRIDQANQRATKML
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Best Local Similarity
Matches 16; Conserv
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CITY: FORT DETRICK

CONTRY: WARNAND

COUNTRY: UGA

ZIP: 21702-501

ZIP: 21702-501

ZIP: 21702-502

COMPUTER RADALE FORM:

COMPUTER PRADALE FORM:

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COMPUTER PRADALE FORM:

COMPUTER: ADDIS MACINTON 7.0

SOFTWART APPLICATION NATA:

FILING DATE:

ATTONING NATE:

FILING DATE:

ATTONING NATE:

ATTONING NAME:

FILING DATE:

ATTONING NAME:

ATTONING NAME:

FILING DATE:

ATTONING NAME:

ATTONING NA
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Sequence 30, Application US/10948097

Sequence 30, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: BEFRENCE: 66872-040

TITLE OF INVENTION: Determining Clostridial Toxin Activity

TITLE OF INVENTION: UNMBER: US/10/948,097

CURRENT APPLICATION NUMBER: US/10/948,097

NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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  RESULT 2
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Sequence 34, Appl
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Sequence 35, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 1, Appli
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                                                                                                                                                                 April 3, 2006, 15:49:32 ; Search time 6.38532 Seconds (without alignments) 57.210 Million cell updates/sec
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1: /SIDSS/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
2: /SIDSS/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /SIDSS/ptodata/1/pubpaa/USO7 NEW_PUB.pep:*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDSS/ptodata/1/pubpaa/USO7 NEW_PUB.pep:*
7: /SIDSS/ptodata/1/pubpaa/USIO NEW_PUB.pep:*
7: /SIDSS/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
8: /SIDSS/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
                             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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59
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Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
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APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REPERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 30
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Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels
US-11-169-041-225

US-10-948-071-20

US-10-948-097-20

US-10-948-097-61

US-10-948-097-61

US-10-948-097-61

US-10-948-097-61

US-11-195-098-8

US-10-947-071-55

US-10-947-071-55

US-10-948-097-55

US-10-948-097-51

US-10-948-097-51

US-10-947-071-51
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US-10-980-346B-6
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APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Delay Marc
TITLE OF INVENTION: Lanchanide-Based Substrates and Methods
TITLE OF INVENTION: Por Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 16
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APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Glunore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Plucescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 16
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                                                                                                                                         Length 13;
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; Pred. No. 9.7e-06;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 30 LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                            US-10-947-071-32
; Sequence 32, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;

Matches 12; Conservative 0
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Best Local Similarity 100.
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-948-097-32
                                                                              , ORGANISM: Homo sapiens
US-10-948-097-30
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US-10-947-071-32
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                                                            TYPE: PRT
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Sequence 37, Application US/10980346B
Sequence 37, Application US/10980346B
Sequence 37, Application No. US20060024763A1
Sequence 37, Application No. US20060024763A1
GENERAL INFORMATION:
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
TITLE OF INVENTION: of Botulinum Neurotoxins
TITLE OF INVENTION NUMBER: US/10/980,346B
CURRENT PAPLICATION NUMBER: US/10/980,346B
CURRENT PILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 55
SOFTWARE PATENTIAL OF SEQ ID NOS: 55
SOFTWARE PATENTIAL OF SEQ ID NOS: 55
SEQ ID NO 37
LENGTH: 17
                                                                                                                                                                                                                                                                     APPLICANT: LOS Alamos National Laboratory
APPLICANT: LOS Alamos National Laboratory
APPLICANT: Schmidt, Jurgen G., et al.
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
TITLE OF INVENTION: of Botulinum Neurotoxins
FILE REPERENCE: 8-102,313
CURRENT APPLICATION NUMBER: US/10/980,346B
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 17
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NAME/KEY: MISC_FEATURE
LOCATION: (1)..(17)
OTHER INFORMATION: amide bound at one end of the peptide
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100.0%; Pred. No. 1.3e-05;
:ive 0; Mismatches 0;
                                                                                                                                                                                                ; Sequence 6, Application US/10980346B; Publication No. US20060024763A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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1 RIDEANORATKM 12
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Matches 12; Conservative
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TYPE: PRT

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APPLICANT: Glimore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Ackide Marc
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APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Dudley J.
APPLICANT: Glimce, Marcella
APPLICANT: Glimce, Marcella
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
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APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
CURRENT FILING DATE: 2004-09-22
CURRENT FILING DATE: SOG-22
CURRENT FILING DATE: AND NOS: 96
SOFTWARE: FASELSEQ for Windows Version 4.0
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100.0%; Score 59; DB 6; Length 17
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-948-097-34
; Sequence 34, Application US/10948097
; Publication No. US/2060063222A1
; GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-10-948-097-34
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ORGANISM: Homo sapiens
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LENGTH: 17
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                                                                                                                                                 Sequence 33 Application US/10947071
; Sequence 33 Application US/2060063221A1
; Publication No. US2060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
; APPLICANT: Aoki, Kei Roger
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: Lanthanide Clostridial Toxin Activity
; TITLE OF INVENTION: Lanthanide Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
LEATH: 17
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APPLICANT: Williams, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
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100.0%; Pred. No. 1.3e-05;
/ative 0; Mismatches 0; Indels
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100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels
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US-10-948-097-33
US-10-948-097-33
Sequence 33, Application US/10948097
Publication No. US20060063222A1
GENERAL INFORMATION:
APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-947-071-34; Sequence 34, Application US/10947071; Publication No. US20060063221A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 12; Conservative
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ORGANISM: Homo sapiens
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US-10-947-071-33
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Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Acki, Kein Roger
; TITLE OF INVENTION: Lance
; APPLICANT: Acki, Rea Roger
; TITLE OF INVENTION: Lance
; APPLICANT: Acki, Roger
; TITLE OF INVENTION: Lance
; APPLICANT: Acki, Marc
; TITLE OF INVENTION: Lance
; APPLICANT: Acki, War
; TITLE OF INVENTION: Lance
; TITLE OF INVENTION: Lance
; TITLE OF INVENTION NUMBER: US/10/947,071
; CURRENT APPLICANTON NUMBER: US/10/947,071
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
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US-10-94-071-41

Sequence 41, Application US/10947071

Sequence 41, Application US/10947071

Sublication No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: Lanthaning Clostridial Toxin Activity

FILE REFERENCE: 66872-043

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 12; Conservative 0; Mismatches 0;
Mismatches
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12; Conservative
                                                1 RIDEANORATKM 12
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Matches 12; Conserv
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US-10-947-071-40
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LENGTH: 33
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Sequence 36, Application US/10947071

Publication No. US20060063221A1

Publication No. US20060063221A1

General Information:

APPLICANT: Williams, Dudley J.

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: For Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SEQ ID NO 36

LENGTH: 33

TYPE: PRT

TYPE: PRT

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APPLICANT: Williams Dudley J.
APPLICANT: Williams Dudley J.
APPLICANT: Williams Dudley J.
APPLICANT: Glinore, Marcella
APPLICANT: Gteward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Pluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICANTON NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 18
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Pred. No. 2.8e-05;
                                                                                                                                                                      ; Score 59; DB 6; Length 18; ; Pred. No. 1.4e-05; 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-947-071-35
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US-10-948-097-35
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US-10-947-071-36
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CORGANISM: Homo sapiens
US-09-942-098-27
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ORGANISM: Homo sapiens
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Sequence 27,
Sequence 29,
Sequence 91,
Sequence 94,
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Sequence 54,
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Sequence 31,
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Sequence 32,
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-942-098-91

US-09-942-098-31

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; Sequence 27, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Steward, Lance E.
; APPLICANT: Application Steward, Lance E.
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; TILE REFERENCE: P-AR 4009/942,098
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FSSESEQ for Windows Version 4.0
; SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 59; DB 3; Length 13; 100.0%; Pred. No. 0.00044; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Sceward, Lance E.

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Sercityee A/B Toxins

FILE OF INVENTION: Sercityee A/B Toxins

FILE OF INVENTION WHBER: US/09/942,024

CURRENT FILING DATE: 201-08-28

CURRENT FILING DATE: 201-08-28

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 27
US-09-942-024-85
US-09-942-024-92
US-09-942-098-85
US-09-942-098-95
US-09-942-098-95
US-09-942-098-93
US-09-942-098-93
US-09-942-098-98
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US-09-942-098-99
US-09-942-098-99
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LOCATION: 16 -
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
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Sequence 29, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Pernandez-Salas, Ester

APPLICANT: Pernandez-Salas, Ester

APPLICANT: APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Fret Protease Assays For Botulinum

TITLE OF INVENTION: Servoype A/E Toxins

TITLE OF SEQUENCE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fere Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT APPLICATION NUMBER: US/09/942,024
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91
LENGTH: 16
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100.0%; Score 59; DB 3; I
Best Local Similarity 100.0%; Fred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 91, Application US/09942024; Publication No. US20030143650A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RIDEANORATKM 12
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US-09-942-024-29
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Best Local Similarity
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| Publication No. US20050100973A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. |
| APPLICANT: Steward, Lance E. |
| TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay |
| TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay |
| TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay |
| TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay |
| TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay |
| TITLE OF INVENTION: GFP-SANP26 Fluorescence Release Assay |
| TITLE OF INVENTION: GFP-SANP26 Fluorescence Release Assay |
| TITLE OF INVENTION NUMBER: US/04-08-13 |
| CURRENT FILING DATE: 2004-08-13 |
| PRIOR FILING DATE: 2001-08-28 |
| NUMBER OF SEQ ID NOS: 113 |
| SEQ ID NO 27 |
| LENGTH: 13 |
| LENGTH: TITLE OF THE OFFICE OFFICE OFFI |
| TENGTH: 13 |
| LENGTH: 14 |
| LENGTH: 14 |
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| Sequence 49, Application US/10261161
| Publication No. US20040072270A1
| Publication No. US20040072270A1
| Publication No. US20040072270A1
| Publication No. US20040072270A1
| APPLICANT: Fernandez-Salas, Ester
| APPLICANT: Acki, Kel Roger
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
| TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxi
| FILE REFERENCE: P-AR 4804
| CURRENT APPLICATION NUMBER: US/10/261,161
| CURRENT FILING DATE: 2002-09-27
| NUMBER OF SEQ ID NOS: 109
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 4; Length 13; 100.0%; Pred. No. 0.00044;
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                         100.0%; Score 59; DB 3; Length 13; 100.0%; Pred. No. 0.00044;
                                                                                           0; Indels
                                                                                           0; Mismatches
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          Query Match
Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
                                                                                                                                                                                                        1 RIDEANQRATKM 12
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CORGANISM: Homo sapiens
US-10-261-161-49
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US-10-917-844-27
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ch 100.0%; Score 59; DB 3; Length 16; Similarity 100.0%; Pred. No. 0.00055; 12; Conservative 0; Mismatches 0; Indels
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US-09-942-024-94
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2 RIDEANQRATKM 13

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RESULT 5

FEATURE:

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US-09-942-098-94

Sequence 94, Application US/09942098

Sequence 94, Application US/09942098

Publication No. US20030143651A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: April Kei Roger

TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Fret Protease
FILE REPRENCE: P-AR 4802

CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SEQ ID NOS: 96

SEQ ID NOS: 96

SEQ ID NOS: 96

SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels
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           APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger,
TITLE OF INVENTION: Fret Proctease Assays For Clostridial
TITLE OP INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SSQ ID NO 91
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1 -
OTHER INFORMATION: Xaa=fluorescein-modified lysine
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100.0%; Pred. No. 0.00055;
tive 0; Mismatches 0;
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OTHER INFORMATION: Xaa-DABCYL modified lysine NAME/KEY: MOD_RES
LOCATION: 16
OTHER INFORMATION: Xaa-EDANS modified glutamate NAME/KEY: ANDAILON: (0)...(0)
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; OTHER INFORMATION: at the C-terminal US-09-942-098-94
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OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
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OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
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; OTHER INFORMATION: at the C-terminal US-09-942-098-91
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
  APPLICANT: Steward, Lance E.
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LOCATION: 16
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Sequence 20, Application Wo. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REPERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT APPLICATION NUMBER: 2001-08-28
NUMBER OF ESC ID NOS: 96
SOFTWARE: FattSEQ for Windows Version 4.0
SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 3; Length 16; 100.0%; Pred. No. 0.00055; tive 0; Mismatches 0; Indels
Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward. Lance E.
APPLICANT: Fernandez-Salae, Ester
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serocype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 94
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa-DABCYL modified lysine
NAME/KEY: MOD_RES
LOCATION: 16
OTHER INFORMATION: Xaa=EDANS modified glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: at the C-terminal US-09-942-024-94
                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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CORGANISM: Homo sapiens
US-09-942-098-29
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1 RIDEANQRATKM 12

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; Sequence 91, Application US/09942098 ; Publication No. US20030143651A1 ; GENERAL INFORMATION:

US-09-942-098-91

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Gaps

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; APPLICANT: Aoki, Kei R.
; TILE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TILE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE PEFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRI CRANGE Sapiens
US-10-917-844-29
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US-09-942-024-31

US-09-942-024-31

US-09-942-024-31

Sequence 31, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Formandez-Salas, Ester

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Fret Protease Assays For Botulinum

TITLE OF INVENTION: Serctype A/E Toxins

FILE REFERENCE: P-AR 4803

CURRENT FILING NUMBER: US/09/942,024

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 31

LENGTH: 17

TYPE: PRT
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| Sequence 30, Application US/09942024
| Publication No. US20030143650A1
| Publication No. US20030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 59; DB 5; 100.0%; Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100, nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-942-024-30
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LENGTH: 17
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Matches
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Sequence 51, Application US/10261161

Sequence 51, Application US/10261161

Sequence 51, Application US/10261161

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: APPLICANT: Call-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AA 4804

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SOCTION SEQ ID NOS: 109

SEQ ID NO SI

LENGTH: 16
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| Sequence 67, Application US/10261161 |
| Publication No. US20040072270A1 |
| GENERAL INFORMATION: |
| APPLICANT: Fernandez-Salas, Ester |
| APPLICANT: Ferward, Lance E. |
| APPLICANT: Acki, Kei Roger |
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy |
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy |
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy |
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy |
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy |
| TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy |
| TITLE OF INVENTION: 2002-09-27 |
| WUMBER OF SEQ ID NOS: 109 |
| SEQ ID NO 67 |
| LENGTH: 16 |
| LENGTH:
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100.0%; Score 59; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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              , ORGANISM: Homo sapiens
US-10-261-161-51
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0; Gaps
                                                          Query Match 100.0%; Score 59; DB 3; Length 17; Best Local Similarity 100.0%; Pred. No. 0.00058; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                           1 RIDEANQRATKM 12
|||||||||||||||6
6 RIDEANQRATKM 17
, ORGANISM: Homo sapiens
US-09-942-024-31
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Search completed: April 3, 2006, 15:57:05 Job time : 51.633 secs

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Matches
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Sequence 49, Appli
Sequence 17, Appli
Sequence 37, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
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Sequence 10, Appli
Sequence 11, Appli
Sequence 2, Appli
                                                                            April 3, 2006, 15:31:39 ; Search time 9.57798 Seconds (without alignments) 103.582 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*
.: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-743-8948-1

US-08-743-8948-19

US-08-819-286-9

US-08-819-286-9

US-08-819-286-4

US-08-19-286-4

US-09-534-572-10

US-09-945-172-10

US-09-945-186-1

US-09-948-11

US-08-33-985-18

US-08-33-985-18

US-08-743-8948-17

US-08-743-8948-7

US-08-743-8948-1

US-08-743-8948-1
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                                                                                                                                                                                                                           572060 seqs, 82675679 residues
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59
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Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Sequence 1, Application US/09976535A

Patent No. 6564006

GENERAL INFORMATION:
APPLICANT: Shine, Nancy R.
APPLICANT: Crawford, Karen R.
APPLICANT: Eaton, Linda J.
TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol);
TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
TILLE OF INVENTION: US/09/976,535A
CURRENT APPLICATION NUMBER: US/09/976,535A
CURRENT FILING DATE: 2001-10-12
SOFTWARE: Patentin version 3.1
SEQ. ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/08743894B

Sequence 49, Application US/08743894B

Patent No. 5965699

Patent No. 5965699

GENERAL INFORMATION:

APPLICANT: Maren A. Bostian

TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin from TITLE OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSES: MCMR-JA Attn:John Moran-Patent Atty

STREET: USA MEMC - 504 Scott Street

CITY: FORT DETRICK

STATES: MARYLAND
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100.0%; Pred. No. 7.8e-05;
US-09-962-360B-8
US-08-743-894B-27
US-08-743-894B-33
US-08-743-894B-33
US-08-743-894B-41
US-08-743-894B-39
US-08-743-894B-24
US-08-743-894B-24
US-08-743-894B-25
US-08-743-894B-25
US-08-743-894B-29
US-08-743-894B-36
US-08-743-894B-30
US-08-743-894B-30
US-08-743-894B-30
US-08-743-894B-30
US-08-743-894B-30
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ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
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12; Conserv
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; TYPE: PRT
; ORGANISM: human
US-09-976-535A-1
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US-08-743-894B-49
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APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fro
TITLE OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEB: MCR.JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
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                                                                100.0%; Score 59; DB 1; Length 17; 100.0%; Pred. No. 0.00011; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIF: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION DATA:
PRING APPLICATION DATA:
FILING DATE:
FILING DATE: ROWERE:
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                                                                                                                                                                                                                                                                                           US-08-743-894B-19; Sequence 19, Application US/08743894B; Patent No. 5965699; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION UNDRER: 34,616
REFERENCE/DOCKET 10VMBER:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: James J. Schmidt
                                                    Query Match
Best Local Similarity 100.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
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                                                                                                                                                            1 RIDEANORATKM 12
                                                                                                                                                                                                      5 RIDEANORATKM 16
    ; TOPOLOGY: Linear
US-08-743-894B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 12; Conserv
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US-08-743-894B-37
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Patent No. 5965699
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Green A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STRET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
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SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2665
TELEFAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LEMOTH: 16 antino acids
TYPE: amino acid sequence
STREADDENNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTR: USA
ZIP: 21702-5012
COUNTR: USA
ZIP: 21702-5012
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FLING DATE: NO. 5965699ember 6, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 619-2065
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 amino acids
TYPE: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RIDEANQRATKM 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-743-894B-49
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Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION:
FEPTIOE INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 59; DB 2; Length 20; 100.0%; Pred. No. 0.00013; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/ABENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/678-509
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acid
STRANDEDNESS: not relevant
TYPE: amino acid
STRANDEDNESS: not relevant
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07345
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-08-819-286-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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         APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCRR-JA Attn:John Moran-Patent Atty
STREET: USA MEMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
COUNTRY: USA
MEDIUM TYPE: Flopy disk
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Apple Maxintosh
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Sequence 6. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PERFIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STRETT: 4225 Executive Square, Suite 1400
CITY: La Jolla
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100.0%; Pred. No. 0.00011;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
COMPUTER TEADABLE FORM:
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/743,894B FILING DATE: NO. 5965699ember 6, 1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEFOMNICATION INFORMATION:
TELEFOMNICATION INFORMATION:
TELEFAX: (301) 619-7714
; INFORMATION FOR SEG ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RIDEANORATKM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S RIDEANORATKM 16
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-743-894B-37
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US-08-819-286-9
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1100 New York Ave., N.W., Suite 600
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APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09015960 Patent No. 6043042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
                                                                                                                                                                                                                                                                                                                                                      NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 15F TELECOMMUNICATION: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2543
INPORATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC
CCUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    202-371-2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 RIDEANORATKM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                         20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-015-960-10
                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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    Gaps
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Sequence 4, Application US/08819286
Sequence 4, Application US/08819286
Sequence 4, Application US/08819286
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REPRENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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APPLICATION NUMBER: US/08/819,286
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Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
  12; Conservative
                                                                             11 RIDEANORATKW 22
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                                        1 RIDEANORATKM 12
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                             JS-08-819-286-4
    Matches
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F: 1100 New York Ave., N.W., Suite 600
Washington
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INPORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-09-534-572-10
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Sequence 10. Application US/09534572

GENERAL INFORMATION:
APPLICANT: Alone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Odinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CONTY: Washington
CONTY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 2; Length 70; 100.0%; Pred. No. 0.00052;
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COUNTRY: USA
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGBNT INFORMATION:
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TRILECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 12600
TRILECOMMUNICATION INFORMATION:
RESERVENCE DOCKET NUMBER: 1581.0120003
TRILECOMMUNICATION INFORMATION:
TRILECOMMUNICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
       NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAS: 202-371-2543
INFORMATION FOR SEQ ID No: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 aming acids
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Best Local Similarity 100.
Matches 12; Conservative
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; MOLECULE TYPE: peptide
US-09-015-960-10
                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
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APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Heartoxins
FILE REPERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US 69/9962,360B
CURRENT PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
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Sequence 18, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 59; DB 2; Length 116; 100.0%; Pred. No. 0.00092; ive 0; Mismatches 0; Indels
  Length 70;
                                                Indele
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; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11
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ZIP: 94306

COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                   RESULT 12
US-09-962-360B-11
Sequence 11, Application US/09962360B
; Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 100.
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                                                                                                   1 RIDEANQRATKM 12
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) ORGANISM: Human
US-09-949-016-6311
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Batent No. 615904

GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 1; Length 206; 100.0%; Pred. No. 0.0018;
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ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/819,286
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/ABENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                     ATTORNEY/AGENT INPORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEFANDE: (415) 324-0880
TELEFANDE: (415) 324-0880
TELEFANCE (415) 324-0800
TELEFANCE (415) 324-0800
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 12; Conservative
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FILING DATE:
CLASSIFICATION: 435
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STRANDEDNESS: not
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Db 191 RIDBANGRATEM 202

RESULT 15
US-09-949-016-6311
US-09-949-016-6311
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US-09-949-016-6311
US-09-949-016-6311
US-09-949-016-6311
US-09-949-016
USERVATE INTROPARTION: WHITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF PILLE OF INVENTION: WHITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: 60/241,755
USENTED PRIOR PILLING DATE: 2000-10-20
UNDERNY PILLING DATE: 2000-10-20
UNDERNY PILLING DATE: 2000-10-00
UNDERNY PILLIN
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RESULT
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macaca fasc
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brachydanio
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brachydanio
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brachydanio
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Q488b5 tetraodon n
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brachydanio
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homo sapien
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pan troglod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
                                                                                       April 3, 2006, 15:27:42; Search time 61.8716 Seconds (without alignments) 136.837 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4SBB5_TETNG
Q9CM34_MACFA
Q6FC84_BRARE
SNZ5B_CARAU
093579_BRARE
Q6FC54_BRARE
Q70536_BRARE
Q70536_BRARE
Q77566_BRARE
Q77566_BRARE
Q77566_BRARE
SNP25_G1ICK
SNP25_G1ICK
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PONPY
MACFA
CARAU
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MOUSE
PANTR
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                                                                                                                                               US-09-942-098-2_COPY_191_202
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
                                                              - protein search, using sw model
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05R6U7_1
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OSUOBS
OSNVGS
OSNVK3
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
                                                                                                                                                                                     1 RIDEANQRATKM 12
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22003330336
220064
22006
22006
22006
22006
21086
21086
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21086
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Match 1
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Perfect score:
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                                                                 OM protein
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RX MEDLINE-99057281; PubMed-9843147;

RX MEDLINE-99057281; PubMed-9843147;

RX MEDLINE-99057281; PubMed-9843147;

RX Atsinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,

RA Larhammar D.;

Larhammar D.;

Larhammar D.;

RT comparison of paralogous linkage protein Snap25 in zebrafish:

RY comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage. i.;

T. Neurosci. Res. 54:563-573 (1998).

RY ENBL; AF091593; AAC64289.1; -; mRNA.

RYSP; O87354; LAA.

RYSP; O87354; J.LAA.

RYSP; O87354; LAA.

RYSP; O93578; 49-122.

RASHED-980526-6468; snap22a.

RO; GO:0019717; C:synaptosome; IEA.

GO; GO:00103700; F:transcription factor activity; IEA.

GO; GO:00103700; F:transcription factor activity; IEA.

GO; GO:00103700; F:transcription of transcription, DNA-dependent; IEA.

RYSP; O87555; P:regulation of transcription, DNA-dependent; IEA.

RYSP; RYSP; RYSPS; RYS
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095578 BRAKE PRELIMINARY; PRT; 124 AA.
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 26, Last annotation update)
01-NOM-2004 (TrEMBLrel. 26, Last annotation update)
Synaptosome-associated protein 25.1 (Fragment).
Name-snap25a; Synonyms=Snap;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostrebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostratiophysi; Cypriniformes;
NCBI_TaxID=7955;
                               xenobne
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NON TER 1 1
SEQÜENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;
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100.0%; Pred. No. 0.0086;
ive 0; Mismatches 0;
Q4REP6_TETNG
Q640W4_XENLA
Q640W4_XENLA
Q8AXW1_XENLA
SNP25_TORWA
Q8735_LOLPE
Q8 G9G6_LYMST
Q8 G9G6_LYMST
Q8 G9G41_9PSED
Q85431_9PSED
Q85440_PSETO
Q85440_PSETO
Q8517_PYRAE
Q8517_PYRAE
Q8517_PYRAE
Q8517_PYRAE
Q8517_PYRAE
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SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
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Best Local Similarity 100.
Matches 12; Conservative
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SMR; Q9GM34; 68-141
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Bemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Relis M., Volff JM., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
I. Nature 431:946-957(2004).
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OBADA N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
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                                                                                                                                                                 ORFNames=GSTENG00022427001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca
                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14706, whole genome shotgun sequence.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 59; DB 2; Length 134; 100.0%; Pred. No. 0.0093; ive 0; Mismatches 0; Indels
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049852; BAB16738.1; -; mRNA.
HSSP; Q8T384; 1L4A.
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.; CAAE01014706; CAG03117.1; -; Genomic DNA.
леисв 134 AA; 14682 мм; 09109FF243890A8E CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgy
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                          134 AA
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                          PRT;
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Q9GM34;
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                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=99883;
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STRAIN-Wild-type; TISSUB-EPG;

KX STRAIN-Wild-type; TISSUB-EPG;

KX STRAIN-Wild-type; TISSUB-EPG;

KX Strauberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

KRIAUSER R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

KA Altschul S.F.; Zeeberg B., Bucrow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Zeeberg B., Bucrow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Jordan H.; Moore T., Max S.I.; Wang J., Hsieh F.;

A Dopkins R.F.; Jordan H.; Moore T., Max S.I.; Wang J., Hsieh F.;

A Dopkins R.F.; Jordan H.; Morer A.A.; Rubin G.M.; Hong L.;

Raha S.A.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Raha S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.W.;

Raha S.A.; McMan A.; Sodergren B.J.; Lu X.; Gibbs R.A.;

Raha S.A.; Morley K.C.; Mackerchenko Y.; Bouffard G.G.;

Raha S.A.; Morley M.; Sodergren E.D.; Dickson M.C.;

Raha S.A.; Grimwood J.; Schmutz J.; Myers R.M.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gарв
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                    SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
Hypothetical protein; Synaptosome.
SEQUENCE 143 AA; 16043 WW; D625DBAAA0893FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGPC84 BRARE PRELIMINARY; PRT; 198 AA.
Q6PC84;
Q6PC84;
G5-JUL-2004 (TrEMBLrel. 27, Created)
G5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
G5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio)
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T. SNARE.
Pfam; PF00315; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SNART; SM00397; T. SNARE; 2.
PROSITE; PS50192; T. SNARE; 2.
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SMR; Q6PC84; 1-77, 123-196.
ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 RIDEANORATKM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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188 RIDEANORATKM 199
  1 RIDEANQRATKM 12
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                                                                                                                                                                                                                                                                                                      Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                Gaps
                                                                                                                                                                                                                                                               Carassius auratus (Goldfish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
-1- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome.

DOWAIN 19 81 t-SNARE coiled-coil homology 1.

137 199 t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the nerve terminal.
--- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, a granule cells of terbellum.
--- SIMILARITY: Belongs to the SNAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
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Risinger C., Larhammar D.;
"Multiple loci for synapse protein SNAP-25 in the tetraploid
goldfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 1; Length 203; 100.0%; Pred. No. 0.014;
                                    ; Score 59; DB 2; Length 198; ; Pred. No. 0.014; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8DFBBEDBED37D6D7 CRC64;
                22209 MW; 8FED5099A00E1EC0 CRC64;
                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25B (SNAP-25B)
                                                                                                                                                                               203 AA.
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                                                                                                                                                                               PRT;
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22664 MW;
                                         100.0%;
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SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2
                                                                                                                  183 RIDEANORATKM 194
                                                   Local Similarity 100 les 12; Conservative
                                                                                         1 RIDEANQRATKM 12
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                     Cyprinidae; Carassius.
NCBI_TaxID=7957;
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Synaptosome.
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                                                                                                                                                                                                                                                                                                                                                             rissue=Retina
                                                                                                                                                                                                                                                         Name=SNAP-B;
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                                          Query Match
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Matches
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Matches
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"Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                   MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 2; Length 203; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
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Last sequence update)
Last annotation update)
                                                                    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Synaptosome-associated protein 25.2.
Name=snap2bb, Synonyme=Snap;
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203 AA
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000927; T SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF00839; SNAPR; 1.
SMART; SM00397; L SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synaptosome-associated protein 25 b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Neurosci. Res. 54:563-573(1998).
EMBL; AF091594; AAC64290.1; -; mRNA.
HSSP, P60881; 1JTH.
SMR; O93579; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
PRT;
                                            01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6PC54;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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  093579 BRARE PRELIMINARY;
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Conservative

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Name=snap-25;
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S.M., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.W., Wardy D.M., Sodersia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodersen B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
It and mouse cDNA sequences.",
""The proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
-1- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the nerve terminal.
-!- SIMILARITY: Belongs to the SNAP-25 family.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 2; Length 203; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC059469; AAH59469.1; -; mRNA.
SMR; QCFC54; 7-82, 128-201.
ZFIN; ZDB-GRE-990526-392; snap25b.
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01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25A (SNAP-25A)
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00815; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN=Wild-type, TISSUE=Eye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00397; t SNARE; 2.
PROSITE; PS50192; T SNARE; 2.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=SNAP-A;
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P36977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     goldfish.";
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ID SN25A_CP
DT 01-JUN-1
DT 01-JUN-1
DE Synapro-1
DE Synapr
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:000370; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000228; SNAP-25.
InterPro; IPR000727; TSNARE.
Pfam; PF05739; SNARE; 1.
Pfam; PF05739; SNARE; 1.
PMART; SNAND397; T. SNARE; 2.
PROSTIE; PS50192; T. SNARE; 2.
SEQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;
                                                                                                                                                                                     EMBL; L22973; AAA16537.1; -; mRNA.
R1SSP; P13795; U17S.
R1SSP; P13795; U17S.
RNG P13795; U17S.
RICEPPO; IPRO00928; SNAP-25.
RICEPPO; IPRO00727; T_SNARE.
RPG P13795; SNARE.
RPG P13795; SNARE; U.
RPG P13795; SNARE; U.
RPG STTE; PSC 9122; T_SNARE; U.
RPG 11 Multigene family; Repeat; Synaptosome.
RPG 128 Coiled coil; Multigene family; Repeat; Synaptosome.
RPG 128 COILED COIL HOMOLOGY 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rearch 100.0%; Score 59; DB 1; Length 204; Local Similarity 100.0%; Pred. No. 0.014; es 12; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 2; Length 204; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen K., Huang X.H.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJG19993; CAG4071.1; -; mRNA.
SMR; Q705JG; 7-83, 129-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cys-rich.
458BBECFCFC09189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               070516;
05-UIL-2004 (TrEMBLrel. 27, Created)
05-UIL-2004 (TrEMBLrel. 27, Last sequence update)
05-UIL-2004 (TrEMBLrel. 27, Last annotation update)
05-UIL-2004 (TrEMBLrel. 27, Last annotation update)
Synaptosomal-associated protein 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 92 C
204 AA; 22843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LATJA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 RIDEANQRATKM 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RIDEANORATKM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moronidae, Lateolabrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8164;
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Gaps

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Event-Alternative splicing, Named isoforms=2;
Comment=Isoforms differ by the usage of two alternative
homologous exons (5a and 5b) which encode for positions 56 to 94
and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP25 CHICK STANDARD; PRT; 206 AA.
P60878; P13795; P36974; P70558; Q81XK3; Q96FM2; Q9BR45;
P60878; P13795; P36974; P70558; Q81XK3; Q96FM2; Q9BR45;
P60878; P13795; P36974; P70558; Q81XK3; Q96FM2; Q9BR45;
P701-M-1990 (Rel. 13, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated 25 kDa protein) (Super protein) (SUP).
Name-SNAP25; Synonyme-SNAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBDIVIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STXIA. This complex binds CPLXI. Interacts with TRIM9, RIMS1 and SNAP25BP. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity).
ALTERNAIUE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=White leghorn; TISSUE-Retina; MEDLINE=91126080; PubMed=1992470; Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J., Wilson M.C., a conserved cell type-specific protein in nerve terminals coincides with synaptogenesis."; Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of the chicken gene for SNAP-25 reveals duplicated exon encoding distinct isoforms of the protein."; J. Mol. Biol. 233:67-76(1993).
-!- FUNCTION: t-SNARE involved in the molecular regulation of
                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 2; Length 204; 100.0%; Pred. No. 0.014; Cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B)
MEDLINE=93389738; PubMed=8377193;
Bark I.C.;
EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA
                        SMR; Q5TZ65; 7-83, 129-202.
Ensembl; ENSDARG00000020609; Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
                                                                                        G) GO:0019717; C:synaptosome; IEA.
InterPro; IPR00028; SNAP-25.
InterPro; IPR000727; T. SNARE.
Pfam; PF00835; SNAP-25; 1.
Ffam; PF05739; SNARE; 1.
SWART; SM00397; t_SNARE; 2.
                                                                    ZFIN; ZDB-GENE-980526-468; snap25a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P60878-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P60878-1, P13795-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 RIDEANORATKW 200
                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              1 RIDEANORATKM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=SNAP-25b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                                                                                                                                                                                                                                                    Synaptosome
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
61-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Synaptosomal-associated protein (SNAP).
Name=snap25a; Synonyms=CTTDARP0000005590; ORFNames=DKEYP-8F4.6-002;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                        01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
Synaptosomal-associated protein (SNAP).
Name-snap25a; Synonyms=OTTDARPRO00000553; ORFNames=DKEYP-8F4.6-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Cyprinidae; Chordata, Craniata, Vertebrata; Euteleostomi;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
REBL; BX465184; CAR69031.1; -; Genomic_DNA.
REBL; BX450246; CAR1359.1; -; Genomic_DNA.
REMBL; BX455184; CAL13159.1; JOINED; Genomic_DNA.
REMBL; BX465184; CAL13159.1; JOINED; Genomic_DNA.
REMBL; RX465184; CAL13159.1; JOINED; Genomic_DNA.
REMBL; RX6019777; C:8yraptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000928; SNAP-25.
InterPro; RMARE; 1.
REMBL; RX60199; RNARE; 1.
REMBL; RX60199; TANARE; 2.
REMBL; RX60199; TANARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 2; Length 204; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
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Donaldson S.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lovell J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                              Lovell J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BX465184; CAH69032.1; -; Genomic DNA.
EMBL, BX470246; CAI21360.1; -; Genomic DNA.
EMBL, BX470246; CAH69032.1; JOINED; Genomic DNA.
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                                                        204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSTZ65 BRARE PRELIMINARY;
                                                        OSTZ66 BRARE PRELIMINARY;
QSTZ66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 RIDEANORATKM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donaldson S.;
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SEQUENCE Query Match

RESULT 10
G05T266 BRA
DD G05T26
AC G05T26
DD G1-FE
DD G1-

Best Loca Matches

ઠ 셤 BRARE

removed

EMBL; EMBL; EMBL; EMBL;

EMBL; EMBL;

EMBL;

EMBL; EMBL; EMBL; EMBL;

EMBL;

EMBL; EMBL;

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NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3iochem. J. 317:945-954(1996).
                                                                                                                                                                                      terminal protein SNAP-25.";
Gene 139:291-292(1994).
                                                                                                                       I.C., Wilson M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rogers
                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Cleavage (by BONT/E) (By similarity).

Phosphothreonine (By similarity).

Phosphoserine (By similarity).

ERIEEGMDQINKDMKRAEKNLTDLGKPCGLCV -> DRVEE
GMNHINQDMKRAEKNLKDLGKCCGLFI (in isoform

        SNP25 HUMAN
        STANDARD;
        PRT;
        206 AA.

        P60880;
        P13795;
        P36974;
        P70557;
        P70558;
        Q81XK3;
        Q96FM2;
        Q9BR45;

        01-JAN-1990
        (Rel. 13, Created)
        Created)
        Cated)
        O1-FB-1991
        Rel. 13, Last annotation update)

        13-SEP-2005
        (Rel. 48, Last annotation update)
        Synaptosomal-associated protein (SNAP-25)
        (Synaptosomal-associated protein)

        Synaptosomal-associated protein (SUP)
        (SuP)
        Name=SNAR25;
        Synonyms=SNAP;

        Homo sapiens
        (Human)
        (Human)
        Applead

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                                       -i- PTM: Palmitoylared (By similarity).
-i- SIMILARITY: Belongs to the SNAP-25 family.
-i- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Comain 19 81 t-SNARE coiled-coil homology 1.

Comain 140 202 t-SNARE coiled-coil homology 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; 1PR00028; SNAP-25.
InterPro; 1PR000727; T_SNAP-25.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF00739; SNARE; 1.
SMART; PR00379; SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L. 109251; AAA49070.1; JOINED; GENOMIC_DNA.
L. 109256; AAA49070.1; JOINED; GENOMIC_DNA.
L. 109253; AAA49070.1; JOINED; GENOMIC_DNA.
L. 109254; AAA49071.1; -; GENOMIC_DNA.
L. 109254; AAA49071.1; -; GENOMIC_DNA.
L. 109257; AAA49071.1; JOINED; GENOMIC_DNA.
L. 109259; AAA49071.1; JOINED; GENOMIC_DNA.
L. 109259; AAA49071.1; JOINED; GENOMIC_DNA.
L. 109259; AAA49071.1; JOINED; GENOMIC_DNA.
L. 109250; AAA49071.1; JOINED; GENOMIC_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 010018.
                                                                                                                                                                                                                                                                                                                                                                                                                            M57957; AAA49072.1; -; mRNA.
L09253; AAA49070.1; -; Genomic_DNA.
L09254; AAA49070.1; JOINED; Genomic_DNA.
L09259; AAA49070.1; JOINED; Genomic_DNA.
L09259; AAA49070.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 AA; 23315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A37861; A37861.
SMR; P60878; 7-83, 131-204.
           Sequence=VSP 010018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RIDEANQRATKM 12
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les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,

NCBI_TaxID=9606;

AXCOCC GEE DATA TO

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NEULECTILES SEQUENCE LLANGES SCALE GENOWIL UNANI.

RA MEDLINE-21638749; PubMed=11780652; DOI=10.1038/414865a;

RA Deloukas P., Matthews L.H., Aburst U.L., Burton U., Gilbert J.G.R.,

RA Dones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Baailey U.P., Bardes K.N., Bard L.M., Beare D.M.,

RA Baailey O.P., Burd C.P., Blakes K.N., Bard L.M., Beare D.M.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Clamp M., Clark R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,

RA Grafham D.V., Griffithes C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,

RA Mine S.A., Mistry D., Moore M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Mine S.A., Mistry D., Moore M.A., Fluck D.M., Lovell J.D.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

Mining L., Wray P.W., Hubbard T., Purbin R.M., Bentley D.R., Beck S.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams E.,

Whittehead S.L., Whittaker P., Willey D.L., Williams L., Williams E.,

Whittehead S.L., Whittaker P., Willey D.L., Williams L., Williams E.,

Whitting D. Moore M. T., Dorder T., Durbin R.M., Bentley D.R., Beck S.,

Whittehead S.L., Whittaker P., Willey D.L., Williams E.,

Whitting D. Moore M. T., Dorder T., Durbin R.M., Bentley D.R., Beck S.,

Whittehead S.L., Whitteker P., Willey D.L., Williams E.,

Whitting D. Moore M. T., Dorder T., Durbin R.M., Bentley D.R., Beck S.,

Whittehead S.L., Whitteker P., Willey D.L., Williams E., Williams D. W.,

Whittehead S.L., Whitteker P., Willey D.L., Whithey Bentley D.R., Beck S.,

Whittehead S.L., Whitteker P., Willey D.L., Whitehead S.L., Whitehead S.L., Whittehead S.L., Whittehead S.L., Whittehead S.L., Whittehead S.L., Whittehead S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Atapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Marxy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ricksley R.W., Touchman J.W., Green B.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skeletal muscle;
MEDLINE=96332494; PubMed=8760387;
MEDLINE=96332494; PubMed=8760387;
Magadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J., Ward C.W.;
Ward C.W.;
"Insulin-responsive tissues contain the core complex protein SNAP-25 (Synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                           MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=94333829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2;
                                                                                                        Human cDNA clones encoding two different isoforms of the nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                      Zhao N., Hashida H., Takahashi N., Sakaki Y.; "Cloning and sequence analysis of the human SNAP25 cDNA."; Gene 145:313-314(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A).
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H-InvDB;
MIM; 6003
                removed
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EMBL, AF240770; AAF64477.1; -; mRNA. SMR, P60877; 7-83, 131-204. Interpro; IPR000928; SNAP-25. Interpro; IPR00727; T_SNARE. Matches 셤 ઠે This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human 94 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX WITH STX1A; CPLX1 AND VAMP2, AND NWR ANALYSIS.
MEDLINE-21822661; Pubmed=11832227; DOI=10.1016/50896-6273(02)00583-4; Chen X., Tomchick D.K., Kovrigin E., Arac D., Machius M., Suedhof T.C., Rizo J.;
"Three-dimensional structure of the complexin/SNARE complex."; RIMS1, Neuron 33:397-409(2002).

-!- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the neurotransmitter release. May play an important Rosciates with proteins involved in vesicle docking and membrane fusion.

-!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with Event-Alternative splicing, Named isoforms=2; Comment-Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to and differ only in 9 positions out of 39; MIM; 600322; -.
GO; GO:0007269; P:neurotransmitter secretion; NAS.
GO; GO:0001504; P:neurotransmitter uptake; NAS.
GO; 00:0001504; P:negulation of insulin secretion; TAS.
GO; GO:0007268; P:sgnaptic transmission; NAS.
GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE. Sequence=VSP 006186;
--- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, a granule cells of the cerebellum.
--- PTM: Palmitoylated (By similarity).
--- SIMILARITY: Belongs to the SNAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains. Q8IUH5:HIP14; NbExp=1; IntAct=EBI-524785, EBI-524753; ALTERNATIVE PRODUCTS: Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). EMBL, AL023913, CAC34534.1, -; Genomic_DNA.
EMBL, AL023913, CAC34535.1; -; Genomic_DNA.
EMBL, AL023913, CAD56158.1; -; Genomic_DNA.
EMBL, AL023913, CAB42660.1; -; Genomic_DNA.
EMBL, BC010647; AAH10647.1; -; mRNA. Ensembl; ENSG0000132639; Homo sapiens HGNC; HGNC:11132; SNAP25. PIR; I53735; I53735.
PIR; I67823; I67823; I67823; I67823; I67823; I67823; I871; Xraay; C=11-80, D=141-203.
PDB; IXTG; X-ray; B=146-204.
SMR; P60880; 7-83, 131-204. STX1A and VAMP8 (By similarity). EMBL; L19760; AAC37545.1; -; mRNA. EMBL; L19761; AAC37546.1; -; mRNA. EMBL; D21267; BAA22370.1; -; mRNA. IsoId=P60880-2, P13795-2; IsoId=P60880-1, P13795-1; and mouse cDNA sequences."; Sequence=Displayed; HIX0015639; -. I53735, I53735. I67823, I67823. Name=SNAP-25a; Name=SNAP-25b; IntAct; P60880; -INTERACTION:

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                               Phosphothreonine (By similarity).
Phosphoserine (By similarity)
ERIEEGMDQINKDMKEAEKNLTDLGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
Subunt: Part of the SNARE core complex containing SNAP25, VAMP2 and SYRIA. This complex binds CPLX1. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity).
STXIA and VAMP8 (By similarity).
SIMILARITY: Belongs to the SNAP-25 family.
SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP25 MACMU STANDARD; PRT; 206 AA.
P60877; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 13, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 kba protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                          GMNHINODMKEAEKNLKDLGKCCGLFI (in isoform SNAP-25a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Hippocampus;
Jensen M.J., SMITE L.A.;
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates wi proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Pfam; PF00835; SNAP-25; 1.

Pfam; PF05739; SNARE; 1.

SNART; SM00397; t SNARE; 2.

PROSITE; PS50192; T SNARE; 2.

3D-structure; Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat; Synaptosome.

Palmitate; Phosphorylation; Repeat; Synaptosome.

t-SNARE coiled-coil homology 1.

t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 100.0%; Score 59; DB 1; Length 206; Similarity 100.0%; Pred. No. 0.014; 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 82
142 201
202 202
206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_006186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 RIDEANORATKM 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                    140
85
180
138
                                                                                                                                                                                                                                                                                                                                                            MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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STRAIN=C57BL/6J; TISSUE-Medulla oblongata;

X MEDLINE=22354683; PubMed=12466851; DOI=101303 /nature01266;

A MEDLINE=22354683; PubMed=12466851; DOI=101.0139 /nature01266;

A Mikaido I., Osato N., Satto R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Satto R., Suzuki H., Yamanaka I., Kiyosawa H.,

A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
                                                                                                                                                                                                                                                                                                                                               SNP25 MOUSE STANDARD; PRT; 206 AA.
P60879; P13795; P36974; P70557; P70558; QBIXK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 13, Created)
01-FBE-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 kDa protein) (Super protein) (SUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/C;
MEDLINE=9079137; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
MEDLINE=807078377; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M., Bloom F.E., Wilson M.C.;
Bloom F.E., Wilson M.C.;
"The identification of a novel synaptosomal-associated protein, SNAP-"The identification of a novel synaptosomal-associated protein, SNAP-"
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                           Cys-rich.
Cleavage (by BONT/E) (By similarity).
Phosphothreonine (By similarity).
FBED28082A4C86A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ILS, and ISS;
MEDLINE=21363810; PubMed=11471062; DOI=10.1007/s00335-001-1001-x;
Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
"High-throughput sequence identification of gene coding variants
within alcohol-related QTLS.";
                                                                                                                                                                                                                            ;
0
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
                                                                                   t-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
                                                                                                                                                                                          , Score 59, DB 1; Length 206;
, Pred. No. 0.014;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuronal subpopulations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
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    differentially expressed by ner
    Cell Biol. 109:3039-3052(1989).

                                                                                                                                                                    23315 MW;
                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mamm. Genome 12:657-663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Snap25; Synonyms=Snap;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                191 RIDEANORATKM 202
                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                      1 RIDEANQRATKM 12
                                                                                   81
202
92
181
138
187
                                                                                                                                        138 1
187 1
206 AA;
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                      Synaptosome.
DOMAIN
                                                                                                                                        MOD RES
MOD RES
SEQUENCE
                                                                                                              COMPBIAS
                                                                                                  DOMAIN
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NEULIDEOTIDE SEQUENCE LLAKES SCALE FROM 1 (1905FORM SNAF-ZSA).

OSTRAIN-CSTBL/6; TISSUE-EYE:

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feringold B.A., Grouse L.H., Derge J.G.,

Ralausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards C., Garlimon M., Sodergren B.J., Lu K., Gibbs R.A.,

Raha S.S., Calmwood J., Schwutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Colonaration and initial analysis of more than 15,000 full-length human
Ravasi T., Reed J.C., Reed D.J., Raid J.C., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Sercou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Wanger L., Wahlestedt C., Wang Y., Watanabe Y., Walls C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Hyana Z., Zavolan M., Zimmer A., Carnnot P., Hayarsu N., Ahirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3; Hepp R., Cabaniols J.P., Roche P.A.; "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion. SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STXIA. This complex binds CPLXI. Interacts with TRIM9, SNAP2SBP and HGS. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and protein kinase A.";
FEBS Lett. 532:52-56(2002).
-!- FUNCTION: t-SNARE involved in the molecular regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10195194; DOI=10.1038/5673;
Ilardi J.M., Mochida S., Sheng Z.-H.;
"Snapin: a SNARE-associated protein implicated in synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Neurosci. 2:119-124(1999).
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IsoId=P60879-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P60879-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=VSP_010019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=SNAP-25b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmission.";
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
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Cys-rich.

Cys-rich.

Cys-rich.

Phosphothreonine (by PKC and PKA).

Phosphoserine (by PKC).

PRIEEGMOQINKDMEABEKNI.TDLGKECGLCV -> DRVEE

GWNHINQDMEABERNI.KDLGKCCGLFI (in isoform

SNAP-25a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  EMBL; AF483516; AA490790.1; -; mENA.

EMBL; AF483516; AA490790.1; -; mENA.

EMBL; AF483517; AA490790.1; -; mENA.

EMBL; AR78038; BAC37105.1; -; mENA.

EMBL; A37623; A33623.

EMBL; BC018249; AA418249.1; -; mENA.

ENBER, BC01826; C101826.1; -; mENA.

EMBL; MGI; MGI; SNAP.

ENGI; MGI; SNAP.

ENGI; MGI; SNAP.

ENGI; MGI; SNAP.

ENGI; SNAP.

ENGIPE: POSO39; ENARE;

EN
-!- PTM: Palmitoylated (By similarity).
-!- SIMILARITY: Belongs to the SNAP-25 family.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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FBED28082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA; 23315 MW;
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Search completed: April 3, 2006, 15:46:25 Job time : 61.8716 secs

191 RIDEANQRATKM 202

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

April 3, 2006, 15:30:10 ; Search time 6.49541 Seconds (without alignments) 177.756 Million cell updates/sec Run on:

US-09-942-098-2_COPY_191_202 59 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RIDEANQRATKM 12 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		synapse protein SN	synaptosomal-assoc	nerve terminal pro	nerve terminal pro	synaptosomal-assoc	synapse protein -	outer membrane lip	vesicle-membrane t	SNARE protein 23 -	н	.	_	٠,	_			hypothetical prote	н	hypothetical prote	hypothetical prote	transcription regu	cal	tektin Al - sea ur	protein T23E18.18	-	hypothetical prote		hypothetical prote
QI	IS0481	I50480	A37861	153735	167823	A33623	I50552	A33854	JC5297	JC5512	JC5296	T32127	T34187	D84748	T05428	D8488	T17345	S76238	G95369	D72668	AB1996	AE3518	T26205	A46170	A96790	564386	S49376	D83063	T47909
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* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	84.7	64.4	61.0	61.0	61.0	61.0	61.0	59.3	59.3	59.3	59.3	59.3	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6
Score	59	60	59	59	59	59	20	38	36	36	36	36	36	35		35	35	35	34	34	34	34	34	34	34	34	34	34	34
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T08416 S64405	230700 A43607 T16613 RE6085	H97828 B70338	E64504 A24733 S70030	PN0157 PN0158 151912 RRNZ
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30	J W W U	346.2	33 39 41 41	4 4 4 4 C C 4 2

ALIGNMENTS

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synapse protein SNAP-25 - goldfish
Sypeies: Carassius auratus (goldfish)
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150481
R;Risinger, C; Larhammar, D.
R;Risinger, C; Larhammar, D.
R;Atsinger, C; Larhammar, D.
R;Atsinger, C; Larhammar, D.
R;Atcession: 150481
A;Accession: 150481
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Reference number: A503 RIS>
A;Residues: 1-203 RIS>
A;Residues: 1-203 RIS>
A;Residues: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:g349430; PIDN:A;Genetics:
A;Genetics:
RESULT 1
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Length 203; Query Match
100.0%; Score 59; DB 2; I
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 12; Conservative 0; Mismatches 0;

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Gaps

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0; Indels

1 RIDEANQRATKM 12 ઠ 셤

RESULT 2

synapse protein SNAP-25 - goldfish
synapse protein SNAP-25 - goldfish
c;species: Carassius auratus (goldfish)
c;bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
c;bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
c;batesion: I50480
R;Risinger, C; Larhammar, D.
R;Risinger, C; Larhammar, D.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Reference number: A50480
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Coss-references: UNIPROT:P36977; UNIPARC:UPI0000135802; GB:L22973; NID:g349426; PIDN:}

A; Gene: SNAP-25

Query Match Best Loca Matches

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Gaps

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0; Indels

Match 100.0%; Score 59; DB 2; Local Similarity 100.0%; Pred. No. 0.00091; es 12; Conservative 0; Mismatches 0;

Length 204;

RESULT 3

A; Accession: A37861

Query Match

Best Loc

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Gynaptosomal-associated 25K protein - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Musculus (house) (Species: Musculus (house) (Species: Musculus (Musculus )) (Species: Musculus (Musculus )) (Species: Musculus (Musculus )) (Species: Musculus )) (Species: Musculus (Musculus )) (Species: Musculus )) (Species: Musculus )) (Species: Musculus )) (Musculus )) (Musculus
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C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
J;Risinger, C;Blomgvist, A.G.; Lundell, I; Lambertsson, A.; Nassel, D; Pieribone, V.;
J; Diol. Chem. 268, 24408-24414, 1993
A;Reference number: A49513; MulD:94043281; PMID:8226991
A;Reference number: A49513; MulD:94043281; PMID:8226991
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A,Molecule type: mRNA
A,Residues: 1-210 <RISA
A,Cross-references: UNIPROT:P36976; UNIPARC:UP10000135AFE; GB:L22020; NID:g431296; PIDN:?
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C;Species: Pseudomonas aeruginosa
C;Species: Perb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33854; SodWelzer A38288
R;Duchene, M.; Barron, C.; Schwelzer, A.; von Specht, B.U.; Domdey, H.
J. Bacteriol. 171, 4130-4137, 1889
A;Fible: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, sec
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A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI000001103; GB:M22012; GB:X51673; NID:9200
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                                                                                                                                     Length 206;
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                                                                                                                       100.0%; Score 59; DB 2;
100.0%; Pred. No. 0.00092;
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Pred. No. 0.049;
1; Mismatches
                                                                                                                                                                                                                0; Mismatches
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2
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Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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R;Bark, I.C.; Wilson, W.C.
Rene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein A;Reference number: 153735, MUID:94156217; PMID:8112622
                                                                                                                                                                                                                                                                                                         C;Accession: A37861

K;Cateicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.

Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991

A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid

A;Reference number: A37861; MUID:91126080; PMID:1992470
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Rene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: 153735; MUID:94156217; PMID:8112622
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A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
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A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UP10000001103; GB:M57957; NID:g212673; PIDN:
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI000002B3DD; GB:L19760; NID:g307425; PIDN:
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C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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A;Molecule type: mRNA
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A, Map position: 20p11.2-20p11.2
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191 RIDEANQRATKM 202
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Accession: I53735

A; Accession: 153735

Query Match Best Local Similarity Matches 12; Conserv

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A; Gene: GDB: SNAP

A; Accession: 167823

Genetics:

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A;Cross-references: UNIPROT:O16766; UNIPARC:UP100001642E9; EMBL:AF016686; PIDN:AAB66239.1
A;Experimental source: strain Bristol N2; clone R07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Howo sapiens (man)
C;Species: Howo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JG5296
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biochem. Brophys. Res. Commun. 211, 808-812, 1997
Biochem. Biochem. Brophys. Res. Commun. 211, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 ir A;Reference number: JG5296; MUID:97224437; PMID:9070898
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C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cent
                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S; Tamoni, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Oka; Biochem. Biochem. Biochem. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Muncl8c.
A;Reference number: JC5512; MUID:97312558; PMID:9168999
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
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Pred. No. 23;
1; Mismatches 3; Indels
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66.7%;
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                                                      144 RIDIANARAKKL 155
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Matches 8; Conservative
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1 RIDEANORATKM 12
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Matches 8; Conserv
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K.; Lim,
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C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cen
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A,Reference number: A82950; MUID:20437337; PMID:10984043
                                    A; Molecule type: DNA,
A; Residues: 1-83 a CDC.
A; Residues: 1-83 a CDC.
A; Cross-references: UNIPROT: P11221; UNIPARC: UPI000002C273; GB: M25761; NID: G151334; PIDN: A; Cross-references: UNIPROT: P11221; UNIPARC: UPI0000002C273; GB: M25761; NID: G151334; PIDN: R; Cornelis, P: Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube R; Cornelis, P: Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube A; Title: Cloning and analysis of the gene for the major outer membrane lipoprotein from A; Reference number: S04834; MUID: 89313294; PMID: 2473376
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A;Cross-references: UNIPARC:UPI000002C273; GB:AE004712; GB:AE004091; NID:g9948940; PIDN:
A;Experimental source: strain PAO1
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R;Mollinedo, F.; Lazo, P.A.
Biochem. Bjophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23
A;Reference number: JC5296; MUID:97224437; PMID:9070898
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Nature 406, 959-964, 2000
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C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
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A;Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIP:103667)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 158;
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C;Keywords: lipld binding; lipoprotein; membrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F;20-83/Product: lipoprotein I #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 2;
Pred. No. 3.6;
2; Mismatches 1
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70.0%;
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Best Local Similarity 70...
T; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <SAI>
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Gaps

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Score 35; DB 2; Length 331; Pred. No. 57; 4; Mismatches 2; Indels

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hypothetical protein F28A23.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: 13.4pr-1999 #sequence_revision 23.4pr-1999 #text_change 09-Jul-2004
C;Accession: T05428
R;Bevan, M.; WeichBelgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Ne submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15415
A,Recession: T05428
A;Reference number: Z15415
A,Residues: 1-331 < kBV.
A,Gross-references: UNIPROT:049486; UNIPARC:UPI000009E7D4; EMBL:AL021961
A;Residues: 1-331 < kBV.
A;Cross-references: UNIPROT:049486; UNIPARC:UPIOn0009E7D4; EMBL:AL021961
A;Residues: 1-351 < kBV.
A;Introns: 257/1
A;Introns: 257/1
A;Rober: F28A23.160
C;Superfamily: Arabidopsis thaliana hypothetical protein F17M5.80
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Local Similarity 50.0%;
les 6; Conservative
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121 KIEEANQKRLKL 132
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84748
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
N;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Redecule type: DNA
A;Residues: 1-71 <STO>
A;Residues: 1-71 <STO>
A;Coss-references: UNIPROT:023658; UNIPARC:UPI00000A2B44; GB:AE002093; NID:g2253578; PI
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C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 12-Jul-2004
C;Accession: T34187
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A,Gene: CESP:R07C3.10
A,Map position: 2
Asintrons: 20/1; 350/2
C,Superfamily: Caenorhabditis elegans hypothetical protein C32B5.10
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Pred. No. 61;
                                                                                                                                        Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C49H3
A;Reference number: Z21485
A;Accession: T34187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-540 <WUX>
                                                                                                                                   Score 36; DB 2;
Pred. No. 44;
2; Mismatches
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58.3%;
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Best Local Similarity 70.0%;
Matches 7; Conservative 1
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Best Local Similarity 54.5%;
Matches 6; Conservative
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A;Introns: 247/2; 319/2; 393/3
                                                                                                                                     Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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RESULT 15

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April 3, 2006, 15:27:08 ; Search time 61.5413 Seconds (without alignments) 85.675 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                     2443163
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                                                                                                                                                                                                                                                                                                                2443163 seqs, 439378781 residues
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59
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                            OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aae36672 Human SNA	Abw01728 Human SNA	Adm97043 Botulinum	Aea14917 Human SNA	Aay44069 Human SNA	Fret	Fret s		Abw01795 FRET subs	Abw01730 Human SNA	Abw01792 FRET subs	_	Botuli	Human	Human	Human	Aay44021 Amino aci	Abg69065 Human pol	Human	Human	Human	Abw01731 Human SNF		Adm97062 Botulinum
ΩI	AAE36672	ABW01728	ADM97043	AEA14917	AAY44069	AAE36736	AAE36739	AAE36674	ABW01795	ABW01730	ABW01792	ADM97045	ADM97061	AEA14919	AAY44057	AAY44039	AAY44021	ABG69065	AAE36675	AAE36676	ABW01732	ABW01731	ADM97046	ADM97062
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	59	29		29	29	29	59	20	69	65	62	65	65	59	65	29	50	52	65	59	53	53	50	29
Result No.	-	8	m	4	'n	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Adm97047 Botulinum Aea14921 Human SNA Aea14920 Human SNA Aea4647 Human SNA		Fret Fret	ADW01193 FRE1 BLUB ADw01786 FRET BLUB ADw11316 FRET BLUB Adw13111 SNAP 25 P Adw30100 Neurotran	Abw01798 FRET subs Aae36734 Fret subs Abw01790 FRET subs Aae36738 Fret subs Abw01794 FRET subs
8 ADM97047 9 AEA14921 9 AEA14920	AMESOS / AME		7 ABW01793 7 ABW01796 8 ADP13171 2 AAW30100	
17	188	16161	119	8881108
444	,,,,,,		59 100.0 59 100.0 59 100.0	559 100.0 599 100.0 599 100.0
25 27 27 27	3 3 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 2 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	, , , , , , ,) H Q M 4 M

ALIGNMENTS

Human, clostridium toxin, protease activity, botulinum toxin, BoNT, TeNT, tetanus toxin, VAMP, synaptobrevin, SNAP-25, syntaxin, pharmaceutical, AAE36672 standard; peptide; 13 AA. (first entry) Human SNAP-25 peptide #3 WO2003020948-A2 Homo sapiens. 07-AUG-2003 13-MAR-2003. cosmetic. AAE36672; AAE36672

22-AUG-2002; 2002WO-US027145. 28-AUG-2001; 2001US-00942024.

(ALLR) ALLERGAN INC.

Aoki KR; Fernandez-Salas E, Steward LE,

WPI; 2003-290198/28.

Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.

Disclosure; Page 40; 168pp; English.

The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus

RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining clostridial toxin protease activity, by treating sample with
                                                                                     purification
toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin, and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is human SNAP-25 peptide used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 ABW01728 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-2004 (first entry)
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(FERN/) FERNANDEZ-SALAS E.
                                                                                                                                                                                                                                    Conservative
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ses 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ABW01728;
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Matches
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The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial coxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance cransfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell is indicative of clostridial toxin activity. (M1) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (M1) is an automated high-throughput assay. (M1) caduces the need for animal toxicity studies and serves to analyze contacted from a BONTA, BONTA, SONTA, BONTA, BONTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                               clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                            Botulinum toxin substrate recognition sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 49; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aoki KR;
                       ADM97043 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandez-Salas E, Steward LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2003; 2003WO-US028092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2002; 2002US-00261161
                                                                                                                          (first entry)
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1es 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-340456/31
                                                                                                                                                                                                                                                                                                                                      WO2004029576-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxin substrate
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                                                                                                                            01-JUL-2004
                                                                                                                                                                                                                                                                                    Synthetic.
                                                                          ADM97043;
ADM97043
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RESULT

RIDEANORATKM 13

96US-00743894 96US-00743894

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The invention relates to an enzymatic assay for the quantitation of type CC A botulinum toxin, by determining the proteolytic activity of botulinum coxin type A using fluorescamine detection. Botulinum toxin A has neurotoxin type A using fluorescamine detection. Botulinum toxin A has comen between residues 197-198. The method comprises adding an analogue (e.g. between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points, and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured to a partitions. The method is useful for the quantitation of
                                                                                                                                                                                                                                                                                                                                                       Quantitation of type A botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 13-14; 28pp; English.
                                                                                                                                                                                                                                                   Bostian KA, Schmidt JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type A botulinum toxin
                                                                                                                                                                                                      (USSA ) US SEC OF ARMY
                                                                                                                                                                                                                                                                                                        WPI; 1999-579939/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                    06-NOV-1996;
                                                                                                                                                    06-NOV-1996;
US5965699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cosmetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for determining protease activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT) and tetamus neurotoxin (TeNT). The method involves treating with a sample, in solution phase under conditions suitable for clostridial toxin protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, syntaxin) comprising fluorescent protein, first partner of affinity couple and clostridial toxin recognition sequence comprising cleavage site; contacting treated sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated sample. The present sequence is the human SNAP-25 substrate BONT/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                 Human SNAP-25 substrate BoWT/A recognition sequence, SEQ ID NO: 27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (botulinum neurotoxin serotype A) recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SNAP25 (amino acids 187-203) analogue [1-16].
                                                                                                                                                                                                                                      Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 27; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steward LE, Gilmore MA, Aoki KR;
                                       AEA14917 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2004; 2004US-00917844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001US-00942098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALLR ) ALLERGAN SALES INC
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                                                                                                                                      (first entry)
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nes 12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reated sample.
                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                         14-JUL-2005
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                                                                                         AEA14917;
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ARA14917

IID ARA11

XX ARA1

XX ARA1

XX I 14-J

XX Y Neux

XX Homc

XX Ho

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Gaps

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Length 16;

100.0%; Score 59; DB 2; I 100.0%; Pred. No. 0.00027;

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/note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 91 in the sequence listing of the
                                                                                                                                                                                                                                                                                                                                                   /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 91 in the sequence listing of the specification"
                                                                                                                                                                                                                                         Clostridium toxin; protease activity; botulinum toxin; BONT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
0; Indels
                                                                                                                                                                                                               Fret substrate peptide #7 used in the invention.
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                 AAE36736 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification"
                                                                                                                                                                                         (first entry)
    12; Conservative
                                1 RIDEANORATKM 12
                                                          RIDEANQRATKM 16
                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                          07-AUG-2003
                                                                                                                                                                AAE36736;
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Best Loc Matches

ò ద RESULT 5

WO2003020948-A2.

Enzymatic assay, quantitation, type A botulinum neurotoxin, proteolysis, fluorescamine, detection, human, synaptosomal protein, SNAP25,

hydrolysis; amino group

Homo sapiens

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interpressing interpretation to bottlinum serotype A/E (BONT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BONT/E recognition sequence compurising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmedice, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmedics. The present sequence is fret substrate peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                              Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
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Xaa in the sequence shown as SEQ ID NO: 94 in the
sequence listing of the specification"
16
                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to novel clostridium toxin substrates. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Local Similarity 100.0%; Pred. No. 0.00027;
Les 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fret substrate peptide #10 used in the invention.
                                                                                                                                                                                 Aoki KR
                                                                                                                                                                                                                                                                                                                                              Example 1; Page 115; 168pp; English
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                                                                                                                                                                                 Steward LE, Fernandez-Salas E,
                                                       22-AUG-2002; 2002WO-US027145.
                                                                                                 28-AUG-2001; 2001US-00942024
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                                                                                                                                         (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
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Modified-site
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                13-MAR-2003
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Matches
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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BowT/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and spectrum overlapping the emission spectrum of the donor fluorophore and a bowT A or BowT/B recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including botulinum toxins of all serotypes and tetanus coins (TeNT) in a sample including botulinum toxins of all serotypes and tetanus toxins including botulinum toxins of all serotypes and tetanus coins of samples, water samples, cosmetics, tissue samples and beverage or food samples, raw, cooked or processed foods, beverages, animal feed, soil samples, ray are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and cosmetics. The present sequence is fret including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                    Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
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tetanus toxin, VAMP, synaptobrevin, SNAP-25, syntaxin, pharmaceutical;
/note= "EDANS-modified Glutamate; C-terminal amide; Thie residue is given as Xaa in the sequence shown as SEQ ID NO: 94 in the sequence listing of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                       Steward LE, Fernandez-Salas E, Aoki KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 115; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE36674 standard; peptide; 16 AA.
                                                                                                                                                                                    22-AUG-2002; 2002WO-US027145.
                                                                                                                                                                                                                              28-AUG-2001; 2001US-00942024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SNAP-25 peptide #5.
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Best Local Similarity
Matches 12; Conservat
                                                                                                                                                                                                                                                                          (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-290198/28.
                                                                                               WO2003020948-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 AA;
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                                                                                                                                          13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE36674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cosmetic.
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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                    Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetamus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 59; DB 7; Length 16; 100.0%; Pred. No. 0.00027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SNAP-25 BoNT/A recognition peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                         Aoki KR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 29; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fernandez-Salas E,
                                                                                                                                                                                                                                                                            Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001US-00942098.
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                                                                     28-AUG-2001; 2001US-00942098
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FERNANDEZ-SALAS I
AOKI K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100 les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RIDEANQRATKM 14
                                                                                                                                                                      (STEW) STEWARD L E.
(FERN/) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
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                        31-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention further relates to novel closuring most states to the donor insubstaces. The present invention further relates to botulinum serotype A/E (BONN/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (Synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the procease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast camples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification or manner o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                               Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to novel clostridium toxin substrates. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; PRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRST substrate #8 to analyse proteolytic activity of botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "EDANS labelled glutamate; C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 6; 1
100.0%; Pred. No. 0.00027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                      Aoki KR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNAP-25 peptide used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 40; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABW01795 standard; peptide; 16 AA.
                                                                                                                                                                                                                                      Fernandez-Salas E,
                                                                                22-AUG-2002; 2002WO-US027145
                                                                                                                                   28-AUG-2001; 2001US-00942024
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Les 12; Conservative
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                                                                                                                                                                                      ALLR ) ALLERGAN INC
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Modified-site
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                                                                                                                                                                                                                                      Steward LE,
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Length 16; 0; Indels

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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Tetramethylrhodamine labelled lysine; C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulnum toxin. This substrate is used in the exemplification of the invention
                                        The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is human SNAP-25 SONT/A (botulinum neurotoxin serotype A) recognition
                                                                                                                                                                                                                                                                                                                                                                                                                         FRET substrate #5 to analyse proteolytic activity of botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridial toxin, protease activity, tetanus toxin, botulinum toxin, FRET; flourescence resonance energy transfer.
                                                                                                                                                               100.0%; Score 59; DB 7; I
100.0%; Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Fluoresceinated lysine"
                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                ABW01792 standard; peptide; 16 AA.
          Disclosure; Page 10; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 29; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fernandez-Salas E,
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                          1 RIDEANQRATKM 12
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FERNANDEZ-SALAS
AOKI K R.
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                   Sequence 16 AA;
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(AOKI/)
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                                                                                                        peptide
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Sequence 16 AA;

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                                                                                                                                                                                                                                                                                                                              Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.
                                                                                                                                                                      clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food
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100.0%; Score 59; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 12; Conservative 0; Mismatches 0; Indels
Score 59; DB 7; Length 16; Pred. No. 0.00027;
                  Indels
                                                                                                                                                     Botulinum toxin substrate recognition sequence #30.
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                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 51; 188pp; English.
                                                                                                                                                                                                                                                                                               Aoki KR
                                                                                                ADM97045 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                Steward LE,
100.0%;
100.0%;
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                                                                                                                                  01-JUL-2004 (first entry)
Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                    1 RIDEANORATKM 12
                                               3 RIDEANQRATKM 14
                                                                                                                                                                                                                                                                              (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                 WPI; 2004-340456/31.
                                                                                                                                                                                                                                                                                               Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxin substrate
                                                                                                                                                                                                         WO2004029576-A2
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                                                                                                                   ADM97045;
                                                                               RESULT 12
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AEA14919 standard; peptide; 16

RESULT 14

AEA14919

AEA14919;

RIDEANQRATKM 16

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The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore constraints resonance clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance created in exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in cresonance energy transfer of the contacted cell is indicative of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (M1) is useful for determining clostridial toxin formulated clostridial toxin cell reduces the need for animal toxicity studies and serves to analyze reduces the need for animal toxicity studies and serves to analyze contacted from a BoNTA, as bonta, solution and protease activity. In the method (M1), the clostridial toxin substrate is a botulinum toxin substrate comprising a BoNTA, BONTA, BONTA, BONTA, BONTA, Cor TENT substrate comprising a BONTA, 
                                                                                                                                                                                                                                                                                                                                                                             clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance
                                                                                                                                                                                                                                                                                                                                Botulinum toxin substrate recognition sequence #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 67; 188pp; English.
                                                                                                                                                                             ADM97061 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                energy transfer of contacted cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steward LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2003; 2003WO-US028092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2002; 2002US-00261161
                                                                                                                                                                                                                                                                                (first entry)
12
                                             RIDEANQRATKM 16
RIDEANQRATKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-340456/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin substrate
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                                                                                                                                                                                                                                                                                01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                ADM97061;
                                                                                                                             RESULT 13
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Aoki KR;

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The present invention relates to a method for determining protesse activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT) and tetanus neurotoxin (TeVRT). The method involves treating with a sample, in solution phase under conditions suitable for clostridial toxin protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, syntaxin) comprising fluorescent protein, first partner of affinity couple and clostridial toxin recognition sequence comprising cleavage site, contacting treated sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis; fluorescamine; detection; human; synaptosomal protein; SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                            Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sample. The present sequence is the human SNAP-25 substrate BONT/A (botulinum neurotoxin serotype A) recognition sequence.
                                                                        Human SNAP-25 substrate BoNT/A recognition sequence, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 59; DB 9; Length 16; 100.0%; Pred. No. 0.00027;
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                                                                                                    Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human SNAP25 (amino acids 187-203) analogue #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 29; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                Aoki KR;
                                                                                                                                                                                                                                    13-AUG-2004; 2004US-00917844.
                                                                                                                                                                                                                                                                      28-AUG-2001; 2001US-00942098.
                                                                                                                                                                                                                                                                                                    (ALLR ) ALLERGAN SALES INC.
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                                              (first entry)
                                                                                                                                                                                                                                                                                                                                  Steward LE, Gilmore MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RIDEANQRATKM 12
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                                                                                                                                                                        JS2005100973-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                treated sample.
                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                       12-MAY-2005.
                                              14-JUL-2005
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12; Conservative

Best Local Similarity

Matches

Query Match

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Gaps

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100.0%; Score 59; DB 8; Length 16; 100.0%; Pred. No. 0.00027; ive 0; Mismatches 0; Indels

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The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum coxin the A botulinum toxin by determining the proteolytic activity of botulinum coxin than the neurotransmitter peptide Subplement and a been shown to cleave the synaptosomal neurotransmitter peptide SNAP25. Detween residues 197-198. The method comprises adding an analogue (e.g. MY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acid 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that character time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measured amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of type A botulinum toxin
                                                                                                                                                                                                                                                                                                                                       Quantitation of type A botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 9; 28pp; English.
                                                                                                                                                           96US-00743894.
                                                                                                                                                                                              96US-00743894.
                                                                                                                                                                                                                                                                  Schmidt JJ;
hydrolysis; amino group.
                                                                                                                                                                                                                                 (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                    WPI; 1999-579939/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 AA;
                                 Homo sapiens.
Synthetic.
                                                                                                                                                           06-NOV-1996;
                                                                                                                                                                                              06-NOV-1996;
                                                                                                                                                                                                                                                                    Bostian KA,
                                                                                     US5965699-A.
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0; Gaps

Search completed: April 3, 2006, 15:36:56 Job time : 61.708 secs

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Sequence 32, Application US/10948097

Sequence 32, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Applicant

APPLICANT: All Robert

TITLE OF INVENTION: Pluorescence Polarization Assays For

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REPERENCE: 66872-040

CURRENT APPLICATION NUMBER: US/10/948,097

NUMBER OF SEQ ID NOS: 96
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RESULT 2
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Sequence 225, App
Sequence 20, Appl
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57.210 Million cell updates/sec
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                                                                                                                                                         April 3, 2006, 15:49:32 ; Search time 8.51376 Seconds
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1: /SIDS5/ptodata/1/pubpaa/US08_NEW PUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US07_NEW PUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07_NEW PUB.pep:*

4: /SIDS5/ptodata/1/pubpaa/NS07_NEW PUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US07_NEW PUB.pep:*

6: /SIDS5/ptodata/1/pubpaa/US10_NEW PUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW PUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US10_NEW PUB.pep:*
                       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-988-097-32
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US-10-980-346B-6
US-10-947-071-33
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Gaps
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APPLICANT: Williams, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Aoki, Kei Roger,
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 32
LENGTH: 16
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US-10-948-097-20
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US-10-947-071-53
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US-10-948-097-55
US-10-948-097-55
US-10-948-097-55
US-10-948-097-67
US-10-947-071-51
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US-10-948-097-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; sequence 32, Application US/10947071; Publication No. US20060063221A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 16; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Marce
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: Lanthanide Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT APLICATION DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FRSESEQ for Windows Version 4.0
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APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Ker Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
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100.0%; Pred. No. 2.9e-08;
tive 0; Mismatches 0;
                                            Query Match
100.0%; Score 79; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                            ; Sequence 33, Application US/10947071; Publication No. US20060063221A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 16; Conservative
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    US-10-980-346B-37
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LENGTH: 17
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Publication No. US20060024763A1
GENERAL INFORMATION:
APPLICANT: Los Alamos National Laboratory
APPLICANT: Schmidt, Jurgen G., et al.
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
TITLE OF INVENTION: of Botulinum Neurotoxins
FILE REPRENCE: S-102,313
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37
IENGTH: 17
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APPLICANT: Schmidt, Jurgen G., et al.
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
TITLE OF INVENTION: Of Botulinum Neurotoxins
FILE REFERENCE: S-102,313
CURRENT PRILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
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OTHER INFORMATION: amide bound at one end of the peptide
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100.0%; Score 79; DB 6; L
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0;
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Pred. No. 2.7e-08;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 32 LENGTH: 16
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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                                                                                                ORGANISM: Homo sapiens
US-10-948-097-32
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Sequence 36, Application US/10947071
; Sequence 36, Application US/10947071
; Dublication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: Lanthanide-Based Substrates
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT APPLICATION NUMBER: US/10/947,071
; NUMBER OF SEQ ID NOS: 101
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US-10-948-097-35

Sequence 35, Application US/10948097

Sublication No. US2006006322A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marcella

APPLICANT: Gilmore, Marcella

APPLICANT: Geward, Lance

APPLICANT: Geward, Lance

APPLICANT: Box, Kei Roger

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-040

CURRENT FILING DATE: 2004-09-22

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 35

LENGTH: 18
                   APPLICANT: Verhagen, Marchapellon Marchapell
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100.0%; Score 79; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3e-08;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Steward, Lance
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ORGANISM: Homo sapiens
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US-10-947-071-35
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US-10-947-071-36
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APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Glumore, Marcella
APPLICANT: Glumore, Marcella
APPLICANT: Glumore, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Flucrescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 17
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APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Glumore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Pluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 33
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; Sequence 34, Application US/10948097
; Publication No. US/2060063222A1
; GENERAL INFORMATION:
                                                                                                                                                   Sequence 33, Application US/10948097; Publication No. US20060063222A1; GENERAL INFORMATION:
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US-10-948-097-34
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US-10-948-097-33
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16; Conservative
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| Sequence 41, Application US/10947071
| Publication No. US20060063221A1
| Publication No. US20060063221A1
| Publication No. US20060063221A1
| APPLICANT: Gilmore, Marcella
| APPLICANT: Steward, Lance
| APPLICANT: Northagen, Marc
| APPLICANT: Steward, Lance
| APPLICANT: Steward, Lance
| APPLICANT: Steward, Lance
| APPLICANT: Solution | Portion | Portion |
| CURRENT APPLICATION NUMBER: US/10/947,071
| WUMBER OF SEQ ID NOS: 101
| SOFTWARE: FASTSEQ for Windows Version 4.0
| SEQ ID NO 41
| LENGTH: 33
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Pred. No. 6.1e-08;
                                                                                                                 Length 33;
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Local Similarity 100.0%; Pred. No. 6.1e-08;
hes 16; Conservative 0; Mismatches 0;
                                                                                                                 Score 79; DB 6;
Pred. No. 6.1e-08;
                                                                                                                                               0; Mismatches
   SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0
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                                                                                                                                                                                                                 14 SNKTRIDEANORATKM 29
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; ORGANISM: Carassius auratus
US-10-947-071-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Carassius auratus
US-10-947-071-40
                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36
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Best Local Similarity
               SEQ ID NO 36
LENGTH: 33
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TYPE: PRT
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Matches
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Sequence 36, Application US/10948097

Sequence 36, Application US/10948097

Publication Word US20060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Steward, L
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Sequence 40, Application US/10948097

Publication No. US2006006322A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

TITLE OF INVENTION: Plucrescence Polarization Assays For

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-040

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FREUSEQ FOR Windows Version 4.0
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100.0%; Score 79; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Score 79; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0;
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67, Appl
29, Appl
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22, Appl
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                                                                                         April 3, 2006, 15:46:49; Search time 68.844 Seconds (without alignments) 97.107 Million cell updates/sec
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Sequence 29,
Sequence 30,
Sequence 31,
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Sequence 29,
Sequence 51,
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Sequence 32,
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cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-942-098-29

US-10-261-161-51

US-10-261-161-67

US-10-917-844-29

US-09-942-024-31

US-09-942-024-31

US-09-942-024-31

US-09-942-098-31

US-10-261-161-52

US-10-261-161-52

US-10-261-161-53

US-10-261-161-53

US-10-261-161-53

US-10-261-161-53

US-10-261-161-54

US-10-917-844-31

US-09-942-098-32

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US-10-917-844-33

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US-09-942-098-98

US-09-942-098-98
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect
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edirentes	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence								
US-09-942-024-37	US-09-942-024-38	US-09-942-098-33	US-09-942-098-37	US-09-942-098-38	US-10-261-161-55	US-10-261-161-59	US-10-261-161-60	US-10-917-844-33	US-10-917-844-37	US-10-917-844-38	US-10-705-857-4	US-10-917-844-112	US-09-962-360B-11	US-10-802-574-11	US-09-942-024-14	US-09-942-098-14	US-10-261-161-7	
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ALIGNMENTS

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; Sequence 29, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Pernandez-Salas, Ester
; APPLICANT: Pernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Frat Protease
; TITLE OF INVENTION: PASA
; TITLE OF INVENTION: PASA
; TITLE REFERENCE: P-AR 4862
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER: OF SEQ ID NOS: 96
; SEQ ID NO 29
; SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 16;
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       Sequence 29, Application US/08942024

| Sequence 29, Application US/08942024
| Publication No. US20030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E.
| APPLICANT: Steward, Lance E.
| APPLICANT: Aoki, Kel Roger
| TITLE OF INVENTION: Fret Protease Assays For Botulinum
| TITLE OF INVENTION: Serotype A/E Toxins
| FILE REFERENCE: P-AR 4803
| CURRENT APPLICATION NUMBER: US/09/942,024
| CURRENT FILING DATE: 2001-08-28
| NUMBER OF SEQ ID NOS: 96
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 29
| LENGTH: 16
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100.0%; Pred. No. 1.5e-06;
tive 0; Mismatches 0;
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) ORGANISM: Homo sapiens

US-09-942-098-29
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US-09-942-024-29
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16; Conserv
US-09-942-024-29
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Matches 16
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; Sequence 29, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION;
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Gilmore, Marcella A.
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REPERENCE: 6892-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR PILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.0
....hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-942-024-30
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US-09-942-024-30
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Bublication No. US20040072270A1

Bublication No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Acki, Kei Roger

ITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 67
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; Publication No. US20040072270A1
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei, Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxi,
; FILE REFRENCE: P-AR 4804
; CURRENT APPLICATION WUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 5:
LENGTH: 16
             100.0%; Score 79; DB 3; Length 16; 100.0%; Pred. No. 1.5e-06;
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100.0%; Pred. No. 1.5e-06;
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100.0%; Score 79; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                         0; Mismatches
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             Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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Matches 16; Conservative
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CORGANISM: Homo sapiens
US-10-261-161-51
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100.0%; Score 79; DB 5; Length 16; 100.0%; Pred. No. 1.5e-06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09942024

Sequence 30, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Formandez-Salas, Ester

TITLE OF INVENTION: Fret Protease Assays For Botulinum

TITLE OF INVENTION: Serctype A/E Toxins

FILE REFERRNCE: P-AR 4803

CURRENT APPLICATION WIMBER: US/09/942,024

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 17
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CURRENT APPLICATION NUMBER: US/09/942,024
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Sequence 2. Application US/10011588

| Sequence 2. Application No. US20020168727A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Leonard
| APPLICANT: Smith, Leonard
| TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
| TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
| FILE REFERENCE: A34796 06725.013
| FILE REFERENCE: A34796 06725.013
| FILE REFERENCE: A34796 06725.013
| FILE REPELICATION NUMBER: 09/910,186
| PRIOR APPLICATION NUMBER: 09/910,186
| PRIOR FILING DATE: 2000-07-20
| PRIOR FILING DATE: 2000-07-20
| PRIOR FILING DATE: 2000-11-06
| PRIOR FILING DATE: 2000-11-06
| PRIOR FILING DATE: 2001-08-09
| NUMBER OF SEQ ID NOS: 47
| SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei Roger.
TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: PAR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
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100.0%; Score 79; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2
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; Sequence 52, Application US/10261161
; Publication No. US20040072270Al
; GENERAL INFORMATION:
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1 SNKTRIDEANORATKM 16
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Best Local Similarity 100.
Marches 16; Conservative
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CORGANISM: Homo sapiens
US-10-261-161-52
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ORGANISM: Human
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US-09-942-098-30

Sequence 30, Application US/09942098

Publication No. US20030143651A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Fernandez-Salas, Ester

TITLE OF INVENTION: Fret Protease Assays For Clostridial

TITLE OF INVENTION: Fret Protease Assays For Clostridial

TITLE REFERENCE: P-AR 4802

CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 17
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Best Local Similarity 100.0%; Score 79; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches n. Talana
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FOR APPLICANT:
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FOR INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT APPLICATION NUMBER: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 31
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100.0%; Score 79; DB 3; Length 17
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
       CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 31
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Best Local Similarity 100.
Matches 16; Conservative
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US-09-942-098-31
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US-09-942-024-31
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Sequence 68, Application US/10261161

Sequence 68, Application US/10261161

Sequence 68, INCORNATION:

APPLICANT: NFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: C211-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT PAPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-0-27

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 68

LENGTH: 17
                                                                                                                   US-10-261-161-53

Sequence 53, Application US/10261161

Sequence 53, Application US/10261161

Sequence 53, Application US/10261161

SENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Cell-Based Fluorescence Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: PARTICON NUMBER: US/10/261,161
CURRENT FILING DATE: 200-09-27
NUMBER OF SEQ ID NOS: 109

SOC ID NO S:
LENGTH: 17
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100.0%; Score 79; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Score 79; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0;
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Publication No. US20050100973A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Gilmore, Marcella A.
1 SNKTRIDEANORATKM 16
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CRGANISM: Homo sapiens
US-10-261-161-53
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APPLICANT: Aoki, Kei R.

TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Activity
FITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
FILE REFERENCE: 66872-044
CURRENT APPLICATION NUMBER: US/10/917,844
CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US 09/942,098
PRIOR PLING DATE: 2004-08-28
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
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APPLICANT: Gilmore, Marcella A.
APPLICANT: Aoki, Kei R.
TITLE OF INVENTION: GFP-SAND25 Fluorescence Release Assay
TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
FILE REFERENCE: 66872-044
CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US 09/942,098
PRIOR FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 79; DB 5; Length 17; Similarity 100.0%; Pred. No. 1.6e-06; 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 79; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 113
SOFTWARE: PaetSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: April 3, 2006, 15:57:05 Job time : 68.844 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-917-844-31
Sequence 31, Application US/10917844
Publication No. US20050100973A1
GENERAL INFORMATION:
APPLICANT: STEWARA
APPLICANT: STEWARA
APPLICANT: STEWARA
APPLICANT: STEWARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SNKTRIDEANORATKM 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-10-917-844-31
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   US-10-917-844-30
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model Run on:

April 3, 2006, 15:31:39 ; Search time 12.7706 Seconds (without alignments) 103.582 Million cell updates/sec US-09-942-098-29 Title: Perfect score:

1 SNKTRIDEANQRATKM 16 Scoring table: Sequence:

572060 seqs, 82675679 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:* Issued Patents AA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl	1ppli	Appl	Appli	Appli	4ppli	Appl	Appl	Appl	Appl	Appl		1, Ap	71, A	Appl	Ann											
	g	49,	7,	37,	6	. ,	4,	10,	10,	10,	11	18,		6311,	10671,	18,	43,	27,	30,	32,	33	38,	19,	24,	25,	28,	23	43
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	a Chaiman
SOFTERES	αı	US-08-743-894B-49	US-08-743-894B-1	US-08-743-894B-37	US-08-819-286-9	US-08-819-286-8	US-08-819-286-4	US-08-760-001-10	US-09-015-960-10	US-09-534-572-10	US-09-962-360B-11	US-08-393-985-18	US-08-819-286-1	US-09-949-016-6311	US-09-949-016-10671	US-08-743-894B-18	US-08-743-894B-43	US-08-743-894B-27	US-08-743-894B-30	US-08-743-894B-32	US-08-743-894B-39	US-08-743-894B-38	US-08-743-894B-19	US-08-743-894B-24	US-08-743-894B-25	US-08-743-894B-28	US-08-743-894B-29	CA_GAGO_CAE GO DIT
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	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	96.2	96.2	94.9	94.9	94.9	94.9	93.7	93.7	93.7	93.7	93.7	93.7	ć
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Appl Appl Appli Appli	Appl Appl Appl	Appl Appl Appl Appl	Appl Appli Appl Appl	Appl Appl Appl
50,	33,	4 6 4 4 4 6 4 7 7 4 6 7	46, 12, 21,	35, 47, 48,
Sequence Sequence Sequence	Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence
US-08-743-894B-50 US-08-743-894B-51 US-08-743-894B-2	US-08-743-894B-26 US-08-743-894B-26 US-08-743-894B-31 US-08-743-894B-33	US-08-743-894B-34 US-08-743-894B-36 US-08-743-894B-44 US-08-743-894B-45	US-08-743-894B-46 US-09-962-360B-8 US-09-962-360B-12 US-08-743-894B-21	US-08-743-894B-35 US-08-743-894B-47 US-08-743-894B-48
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17	17	11 11 11	17 24 116 17	17
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3000	2 6 6 6 4 2 8 4	335 345 345 35 35 35 35 35 35 35 35 35 35 35 35 35	₩ 4 4 ₩ 0 H V	444 640

ALIGNMENTS

US-08-743-8948-49

1 Sequence 49, Application US/08743894B

PRETENT NO. 5956599

PRETENT NO. 5956599

PRETENT S. 5956599

PRETENT OF INVENTION:

APPLICANT: James J. Schmidt

APPLICANT: James J. Schmidt

APPLICANT: Sand A. Bostian

ITILE OF INVENTION: Assay for the Proteclytic Activity of Serotype A Neurotoxin from Serotype C SEQUENCES: 56

CORRESPONDENCE ADDRESS: Some Control of Secotype A Neurotoxin from Service C STATE: WARN-JA Actu: John Moran-Patent Atty

STREET: USA MEMC- 504 Scott Street

CITY: PORT DEFRICK

STATE: MARYLAND

CONTRY: DAY DEFRICK

STATE: MACTOSOF Wachingh

COMPUTER: Apple Macintosh 7.0

SOFTWARE: Microsoft Word 6.0

COMPUTER: Apple Macintosh 7.0

SOFTWARE: Microsoft Word 6.0

CORRESPONDENCE ADDRESS:

MICROSOFT MACHON TOWNER:

PILING DATE: No. 5965699ember 6, 1996

CLARRETTATION NUMBER:

APPLICATION NUMBER:

PILING DATE: No. 435

PRIOR APPLICATION NUMBER:

RESERENCE CHARACTERISTICS:

RESERENCE CHARACTERISTICS:

TELEPHONE: (301) 619-7714

THYPOMATION OF SECONDESS:

TELEPHONE: MICROSOFT WINBER:

TYPE: Amino acid sequence

STRANDENESS: Single

TYPE: Amino acid sequence US-08-743-894B-49

ö Gaps ö Query Match
100.0%; Score 79; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels US-08-743-894B-49

1 SNKTRIDEANORATKW 16

```
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: DEUTOTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STRATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 79; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
CUMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ACCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIPRICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-WAR-1996
ATTOWNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION UNDHER: 34,616
REFERENCE/DOCKET UNDHER:
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08819286
Patent No. 6169074
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Taylor, Stacy L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-743-894B-37
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US-08-819-286-9
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                                                                                                                                                        Sequence 1, Application US/08743894B
Sequence 1, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Asset J. Schmidt
APPLICANT: MARNC - 56
CORRESPONDENCE ADDRESS:
ADDRESSES: MCMR-JA Attn:John Moran-Patent Atty
STRRET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STRRET: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Asren A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: MCMR-JA Attn.John Moran-Patent Atty
STRET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STRET: MARKIAND
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ilarity 100.0%; Pred. No. 1.5e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: USA

ZIP: 21702-5012

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,894B

FILING DATE: No. 5965699@mber 6, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/08743894B Patent No. 5965699 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATORNEY AGENT:
NAME: Charles H. Harris
REGISTRATION UNDRER: 34,616
REFERENCE/DOCKET 134,616
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE GHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SNKTRIDEANORATKM 16
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: Linear
US-08-743-894B-1
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Gaps

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US-08-819-286-4
                                                                                                                                                      COUNTRY:
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Patent No. 6169074

GENERAL INFORMATION:

APPLICANT: Montal, Mauricio
TITLE OF INVENTION: DEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                     Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 79; DB 2; I 100.0%; Pred. No. 2.4e-07;
                                                                                                   Score 79; DB 2; I Pred. No. 1.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/013,599
FILING DATE: 18-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTATION NUMBER: 34,842
REFERRICE/DOCKET NUMBER: 07349/00500
TELECOMMUNICATION INFORMATION:
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                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEO ID NO: 8: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                               1 SNKTRIDEANQRATKM 16
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TYPE: amino acid
STRANDEDNESS: not relev
                                                                                                         Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
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MOLECULE TYPE: peptide
                                   TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-819-286-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92037
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Sequence 4, Application US/08819286; Patent No. 6169074; GENERAL INFORMATION:

RESULT 6 US-08-819-286-4

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APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 4.5 & SECULIVE Square, Sulte 1400
CITY: La Jolla
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; Patent No. 5962637
; Patent Shone, Clifford C. APPLICANT: Shone, Clifford C. APPLICANT: James, Benjamin A. F. APPLICANT: James, Benjamin A. F. TITHE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: R10Py disk
COMPUTER: R50297 disk
COMPUTER: R10Py disk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSTAILON NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFOMMATION:
NAME: TAYLOR, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 619/678-5079
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APPLICATION NUMBER: US/08/760,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 79; DB 2; I
100.0%; Pred. No. 3.6e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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USA
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Gaps

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100.0%; Score 79; DB 2; Length 70; 100.0%; Pred. No. 7.6e-07; ive 0; Mismatches 0; Indels
                                                                Length 70;
                                                                                                          0; Indels
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1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIATE: UC
CUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDTION TYPE: FOLDAY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/09/15,960
PILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: 08/760,001
FILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 30-DEC-1996
PRIOR APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 08-JUN-1995
ATTONENTY/AGENT INFORMATION:
                                                              Query Match 100.0%; Score 79; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-534-572-10

Sequence 10, Application US/09534572

Patent No. 6337386

Patent INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Ouinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Golds
STREET: 1100 New York Ave., N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 SNKTRIDEANORATKM 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
, MOLECULE TYPE: peptide US-09-015-960-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
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STATE:
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Sequence 10, Application US/09015960

Sequence 10, Application US/09015960

Sequence 10, Application

APPLICANT: Shower

APPLICANT: Halls, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Outnin, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSES: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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ZIP: 2005-3934

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
PROMENT APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
ATFORNEY/AGENT INFORMATION:
NAME: ESSENDEL/BOCKET UNBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-2600
           FLIANG MALE: "ACCEPTION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bemond, Robert W.
REGISTRATION NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
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LENGTH: 70 amino acids
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      Herewith
                                                                                                                                                                                                                                                                                                                LENGTH: 70 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 70 amino
TYPE: amino acid
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Sequence 1, Application US/08819286

Batent No. 6169074

GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: fash & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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                                                                                                        Query Match 100.0%; Score 79; DB 1; Length 206; Best Local Similarity 100.0%; Pred. No. 2.6e-06; Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 79; DB 2; I
100.0%; Pred. No. 2.6e-06;
tive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6311, Application US/09949016;
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 SNKTRIDEANQRATKM 202
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         1 SNKTRIDEANQRATKM 16
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Matches 16; Conservative
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                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-09-949-016-6311
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                                                                                                                                                             AFFICANT: Stafford, Robert G.

TITLE OF INVENTION: High Throughput Assays for the Protecolytic Activities of Clostrid
TITLE OF INVENTION: High Throughput Assays for the Protecolytic Activities of Clostrid
TITLE OF INVENTION: Neurotoxins
FILE REPERENCE: 003/224/6AP
CURRENT PILING DATE: 2002-08-19
FRIOR APPLICATION NUMBER: US 60/235,050
FRIOR RILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
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Patent No. 5693476

GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEB: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 79; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECHONNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
         RESULT 10
US-09-962-360B-11
Sequence 11, Application US/09962360B
; Patent No. 6762280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                              APPLICANT: Schmidt, James J.
                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-393-985-18
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US-08-743-894B-18
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Patent No. 5965699
GENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF INVENTION:
CENERAL OF IN
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| Sequence 10671, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| TITLE OF UNCENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WIMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-32
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-0-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 10671
| LENGTH: 219
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PEPLICATION NUMBER: 60/241,755
PRIOR PEPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,468
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 200
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US-09-949-016-10671
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CITY: FORT DETRICK

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Synaptosome
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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length: 2000000000
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pyrobaculum
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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MEDLINE=99057281, PhDMed=9843147;
DDD=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-UNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
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SEQUENCE 124 AA; 13616 MW; 50827DBDB33D958C CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Synaptocome-associated protein 25.1 (Fragment)
Name-enap25a; Synonyms-Snap;
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100.0%; Pred. No. 1.1e-05;
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BRARE
XENLA
TIRME
MOUSE
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Q8ZY72_PYRAE
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SNP23 M
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SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            093578 BRARE PRELIMINARY;
093578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100.
16; Conservative
230
212
212
212
203
204
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Snap25a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=snap25a;
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                          Mountain State No. Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micallon C., Salanouba M., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanouba M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castellia G., Dossat C., Salli Z., Cattolico L., Poulain J., De Berardinis V., Cruade C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Schachter V., Quetier P., Saurin W., Scarpelli C., Wincker P., Lander E.S., Walssenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain parietal lobe;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sudano S., Hashimoto K.;
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                 Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Mammalia, Eucheria, Burachontoglires, Primates, Eucleostomi;
Cercopithecidae, Cercopithecinae; Macaca.
[11]
                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14706, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBE-2004) to the EMBL/GenBank/DDBJ databases.
-!% CAUTION: The sequence shown here is derived from an
-!% EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049852; BAB16738.1; -; mRNA.
HSSP; Q8T384; 1L4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
1; CAAE01014706; CAG03117.1; -; Genomic_DNA.
JENCE 134 AA; 14682 MW; 09109FF243890A8E CRC64;
                           134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNKTRIDEANQRATKM 16
                                                                                                                                                                     ORFNames=GSTENG00022427001;
                      Q4S8B5_TETNG PRELIMINARY;
Q4S8B5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9GM34 MACFA PRELIMINARY;
Q9GM34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 431:946-957(2004)
                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=99883;
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STRAIN=Wild-type TISSUE=Eye;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KI Straubberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

KI Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

N. Hilaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whilaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                   Score 79; DB 2; Length 143;
Pred. No. 1.2e-05;
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Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           Pram; Pr07/39; SNAKE; 1.
SMART; SM00397; t_SNAKE; 1.
PROSITE; PSS50192; T_SNAKE; 1.
Hypothetical protein; Synaptosome.
SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                            100.0%; Scc...
100.0%; Pred. No. 1...
0; Mismatches
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InterPro; IPR000202; SNAP-25.
InterPro; IPR000727; T SNARE.
Pfam; PF00815; SNAP-25; 1.
SMART; SM00197; t SNARE; 2.
PROSITE; PSS0192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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SMR; Q6PC84; 1-77, 123-196.
ZFIN; ZDB-GENE-980526-468; snap25a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
SMR; Q9GM34; 68-141.

GO; GO:0019117; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SNKTRIDEANORATKM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SNKTRIDEANQRATKM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEPC84, BRARE PRELIMINARY; QEPC84, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
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184 SNKTRIDEANQRATKM 199
1 SNKTRIDEANQRATKM 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larhammar D.;
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Q6PC54_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
--- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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Pram; PP05739; SNARE; 1.

SNART; SN00397; t. SNARE; 2.

PROSITE; PS50192; T. C. SNARE; 2.

COLIECT OF TAXABLE COLLEG-COLL homology 1.

COLLEGE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 Cys-rich.
77 N-linked (GlcNAc. .) (Potential)
1185 N-linked (GlcNAc. .) (Potential)
22664 MW, 8DFBBEDBED37D6D7 CRC64;
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIŜSUE=Retina;
MEDLINE=94068448; PubMed=8248151;
Risinger C., Larhammar D.;
"Multiple loci for synapse protein SNAP-25 in the tetraploid
goldfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 79; DB 1; Length 203; 100.0%; Pred. No. 1.8e-05; rive 0; Mismatches 0; Indels
                                                                  Length 198;
                                                                                                            IndelB
                          22209 MW; 8FED5099A00E1EC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acad. Sci. U.S.A. 90:10598-10602(1993).
                                                                  Score 79; DB 2; I
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25B (SNAP-25B)
                                                                                                                                                                                                                                                                                                          203 AA.
                                                                / Match 100.0%; Score 79; DB Local Similarity 100.0%; Pred. No. 1.8 les 16; Conservative 0; Mismatches
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PIR; I50481; I50481.
HSSP; P13795; LSFC.
SMR; P36978; 7-82, 128-201.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
                                                                                                                                                                                                  179 SNKTRIDEANQRATKM 194
                                                                                                                                                        1 SNKTRIDEANORATKM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carassius auratus (Goldfish)
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 16; Conserv
                              198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=SNAP-B;
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P36978;
               Synaptoвоше.
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                                 SEQUENCE
                                                                         Query Match
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                                                                                                                                                                                                                                                                                         CARAU
                                                                                                                   Matches
                                                                                                                                                                                                                                                                RESULT
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"Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";
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Brachydanio rerio (Zebrafish) (Daniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Wild-type; TISSUE=Bye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRL>3.3.CO;2-Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
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                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Synaptosome-associated protein 25.2. Name-snap25b; Synonyms-Snap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 79; DB 2; I 100.0%; Pred. No. 1.8e-05;
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203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Neurosci. Res. 54:563-573 (1998).
EMBL; AF091594; AAC64290.1; -; mRNA.
HSSP; R60881; 107H.
SMR; 093579; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
GO; GO:0019717; C:synaptcsome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF06339; SNAP-25; 1.
SMART; SM0397; L_SNARE; 1.
SMART; SM0397; L_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGPCS4 BRARE PRELIMINARY; PRT; Q6PCS4; 05-JUL-2004 (TrEMBLrel. 27, Created)
PRT;
                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 SNKTRIDEANORATKM 199
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093579_BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID DT TO DT
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Gaps

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Conservative

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Name=snap-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPBIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                removed.
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rabask S.A., McKernan R.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeabey R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopteryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Actinopteryoti, Neopteryoti; Teleostei; Ostariophysi, Cypriniformes, Cyprinidae, Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-I- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the SNAP-25 family.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 79; DB 2; Length 203;
; Pred. No. 1.8e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN-WILd-type; TISSUE-Eye;
Strausberg R.;
Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 AA; 22693 MW; 48D7590DD0C1179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acad. Sci. U.S.A. 90:10598-10602(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25A (SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC059469; AAH59469.1; -; mRNA.
SMR; Q6PC54; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0019717; C:8ynaptoBome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR00077; T.SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Retina;
MEDLINE=94068448; PubMed=8248151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 SNKTRIDEANORATKM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00397; t_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNKTRIDEANQRATKM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the nerve terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=SNAP-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SN25A CARAU
P36977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  goldfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synaptosome
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EmBL; A46199393; CarPodo11.1 -; mRNA.
R EMBL; A46199393; CarPodo11.1 -; mRNA.
R GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
R InterPro; IPR000928; SNAP-25.
R InterPro; IPR000727; T SNARE.
R Pfam; PF00835; SNAP-25; 1.
R Pfam; PF00835; SNARE; 1.
R SMART; SM00397; T SNARE; 2.
R SMART; CM0397; T SNARE; 2.
C SEQUENCE 204 AA; Z2842 MW; 8F77B18D591509B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleosrei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Moronidae; Lateolabrax.
                                                                                                                                                                                 REMBL; L22973; AAA16537.1; -; mRNA.
R HSSP; P19795; J. AAA16537.1; -; mRNA.
R HSSP; P19795; J. NS.
R R; P36977; 7-83, 129-202.
R InterPro; IPR000928; SNAP-25.
R InterPro; IPR0037; T_SNAP.25.
R Pfam; PF065739; SNAP.25; J.
R Pfam; PF065739; SNAP.25; J.
R PROSITE; PS01027; T_SNARE; 2.
R PROMAIN 138 200 t_SNARE coiled-coil homology 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 79; DB 1; Length 204; 100.0%; Pred. No. 1.8e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 79; DB 2; Length 204; 100.0%; Pred. No. 1.8e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cys-rich.
458BBECFCFC09189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Synaptosomal-associated protein 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q705J6;
05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 200 t
85 92 C
204 AA; 22843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 SNKTRIDEANORATKM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 SNKTRIDEANORATKM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNKTRIDEANQRATKM 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LATJA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=SNAP-25a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBL_TaxID=9031;
                                                                                                                                                                                                                                     Synaptoвоще,
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Name-snap25a; Synonyms=OTTDARP0000005590; ORFNames=DKEXP-8F4.6-002;
Brachydanio rerio (Zbrafish) (Danio rerio).
Brkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                     01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Name-snap2sa; Symonyms-OTTDARP00000005563; ORFNames=DKEYP-8F4.6-001;
Brachydanio rerio (Zebrafiah) (Danio rerio).
Brachydanio rerio (Zebrafiah) (Danio rerio).
Cyprinidae; Danio.
NCDI_TaxID=7955;
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; Bx465184; CAH69032.1; -; Genomic_DNA.
EMBL; Bx470246; CAI21360.1; -; Genomic_DNA.
EMBL; Bx470246; CAI21360.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Donaldson S.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX462184; CAL21359.1; -; Genomic_DNA.
EMBL; BX470246; CAL69031.1; JOINED; Genomic_DNA.
EMBL; BX45184; CAL21359.1; JOINED; Genomic_DNA.
EMBL; BX452184; CAL2139.1; JOINED; Genomic_DNA.
EMBL; BX452184; CAL2139.1; JOINED; Genomic_DNA.
EMBL; ENSDARGO0000020609; Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lovell J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    Lovell J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 100.0%; Score 79; DB 2; L. Local Similarity 100.0%; Pred. No. 1.8e-05; hes 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AA
                                                    204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptcosome; IEA.
Interpro; IPR000928; SNAP-25.
Interpro; IPR000727; T_SNARE.
Pfam; PP00815; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNKTRIDEANQRATKM 16
                   56 BRARE
QSTZ66 BRARE PRELIMINARY;
QSTZ66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSTZ65 BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synaptosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
OSTZ65 BRU
1D AC OSTZ7
DT O1-F
DT O1
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               RESULT 10
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"Structure of the chicken gene for SNAP-25 reveals duplicated exon

"Structure of the chicken gene for SNAP-25 reveals duplicated exon

"Structure of the chicken of the protein.";

J. Mol. Biol. 23:67-76(1993).

L. Mol. Biol. 23:67-76(1993).

C. -!- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with complex in involved in vesicle docking and membrane fusion (By similarity).

C. -!- SUBUNIT: Part of the SNARE core complex containing SNAP2; VAMP2

and SYXIA. This complex binds CPLXI. Interacts with TRIM9, RIMS1
and NAMP2 (By similarity).

C. -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bvent=Alternative splicing; Named isoforms=2;
Comment=Isoforms differ by the usage of two alternative
homologous exons (5a and 5b) which encode for positions 56 to 94
and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP25 CHICK STANDARD; PRT; 206 AA.
P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
P601-JAN-1990 (Rel. 13, Created)
10-FBB-1991 (Rel. 17, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
Synaptosomal-associated protein (SUP).
Name-SNARD25; Synonyms-SNAP;
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=White leghorn; TISSUB=Retina;
MEDLINE=91126080; PubMed=1992470;
Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson M.C.;
"Expression of a conserved cell-type-specific protein in nerve terminals coincides with synaptogenesis.";
Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B) MEDLINE=93389738; PubMed=8377193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 79; DB 2; L
100.0%; Pred. No. 1.8e-05;
tive 0; Mismatches 0;
EMBERGE 1 202 202 ENBERGE 202 ENBERGE 202 ENBERGE 202 202 ENBERGE 200000020609; Danio rerio. 2FIN; ZDB-CENE-980626-468; BND25a. GO; GO: 0019717; C:SYNDAPLOSOME; IRA. INTERPRO; IPR000928; SNAP-25. InterPro; IPR000928; SNAP-25. Fram; PF00835; SNAP-25; 1. Fram; PF06935; SNAP-25; 1. Fram; PF06939; SNARE; 1. SWARE; 2. PR05178; PS06179; SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P60878-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SNKTRIDEANQRATKM 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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9

removed

EMBL; EMBL; EMBL;

EMBL; EMBL;

EMBL; EMBL; EMBL; EMBL;

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Straubberg R.L., Feingold E.M., Grouse D.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan R.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                     TISSUBE-Skeletal muscle;
MEDLINE-96332494; PubMed-8760387;
Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
Grugovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
Biochem. J. 317:945-954 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.";
                                     MEDIINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0; Bark I.C., Wilson M.C.; "Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25."; Gene 139:291-292(1994).
                                                                                                                                                                                                        MEDLINE=94333, PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2; Zhao N., Hashida H., Takahashi N., Sakaki Y.; "Cloning and sequence analysis of the human SNAP25 cDNA."; Gene 145:313-314(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B)
                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 414:865-871(2001).
                                                                                                                                                                                             rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ward C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rogers
      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cys-rich.
Cleavage (by BONT/E) (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
ERIEEGHDQINKDMKEAEKNLFDLGKRCGLCV -> DRVEE
GMNHINQDMKEAEKNLKDLGKCGLPI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP525 HUMAN STANDARD; PRT; 206 AA.
P60880; P13795; P56974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 13, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
J5 kba protein) (Super protein) (Sup).
Name=SNARP5; Synonyms=SNAP;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  Sequence-VSP_010018;
--- PTM: Palmitoylated (By similarity).
--- SIMILARITY: Belongs to the SNAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t-SNARE coiled-coil homology 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 79; DB 1; Length 206; ilarity 100.0%; Pred. No. 1.8e-05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000928; SNAP-25.
Interpro; IPR000727; T_SNARE.
Pfam; PF00035; SNAP-25; 1.
SMART; PF05739; SNARE; 1.
SMART; PF05739; T_SNARE; 2.
PROSITE; P550192; T_SNARE; 2.
Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_010018.
FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                7; AAA49070.1; JOINED; Genomic DNA.
1; AAA49070.1; JOINED; Genomic DNA.
1; AAA49070.1; JOINED; Genomic DNA.
6; AAA49070.1; JOINED; Genomic DNA.
3; AAA49071.1; -; Genomic DNA.
4; AAA49071.1; -; Genomic DNA.
4; AAA49071.1; JOINED; Genomic DNA.
4; AAA49071.1; JOINED; Genomic DNA.
5; AAA49071.1; JOINED; Genomic DNA.
6; AAA49071.1; JOINED; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L09252; AAA49071.1; JOINED; Genomic_DNA.
EMBL; L09258; AAA49071.1; JOINED; Genomic_DNA.
EMBL; L09250; AAA49071.1; JOINED; Genomic_DNA.
PIK, A37861; A37861.
                                                                                                                                                                                                                                      EMBL; M57957; AAA49072.1; -; MRNA.
EMBL; L09253; AAA49070.1; -; Genomic_DNA.
EMBL; L09254; AAA49070.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation; Repeat; Synaptosome.
DOMAIN 19 81 t-SNARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA; 23315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 SNKTRIDEANORATKM 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SNKTRIDEANQRATKM 16
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202
92
181
138
187
89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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MOD_RES MOD_RES VARSPLIC

COMPBIAS

DOMAIN

SEQUENCE Query Match

Matches

RESULT 13

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removed.
                              PIR;
PIR;
                               PDB;
                                   MIM;
                                PDB;
            +
             <u>-</u>
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EMBL; AF240770; AAF64477.1; -; mRNA. SMR; P60877; 7-83, 131-204. InterPro; IPR000928; SNAP-25. InterPro; IPR000727; T_SNARE. DOMAIN COMPBIAS SITE MOD_RES MOD_RES VARSPLIC 187 SEQUENCE Query Match removed. HELIX HELIX GRN Matches ð 셤 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human 94 X. RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX WITH STX1A; CPLX1 AND VAMP2, AND NWR ANALYSIS.
MEDLINE-21822661; PubMed=1183227; DOI=10.1016/S0896-6273(02)00583-4; Chen X., Tomchick D.R., Kovrigin B., Arac D., Machius M., Suedhof T.C., Rizo J.;
"Three-dimensional structure of the complexin/SNARE complex."; Neuron 33:397-409(2002).

-!- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STX1A. This complex binds CPLXI. Interacts with TRIM9, RIMSI, SNAP25BP and HGS. Binds STXBEC. Found in a ternary complex with STXIA and VAMP8 (By similarity). QBIUDE:HIPP4; NDExp=1; IntAct=EBI-524785, EBI-524753; ALTERNATIVE PRODUCTS:

Bvent=Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to and differ only in 9 positions out of 39; 00:0007269; p.neurotransmitter secretion; NAS. GO:0001504; P.neurotransmitter uptake; NAS. GO:00050796; p.regulation of insulin secretion; TAS. GO:0007268; P:symaptic transmission; NAS. GO:0016081; p.symaptic vesticle docking during exocytosis; NAS. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) EMBL, AL023913; CAC34534.1; -; Genomic DNA. EMBL, AL023913; CAC34535.1; -; Genomic DNA. EMBL, AL023913; CAD561581.1; -; Genomic DNA. EMBL, AL023913; CAB42660.1; -; Genomic DNA. EMBL, BC010647; AAH10647.1; -; mRNA. IntAct; P66880; -.
Ensembl; ENSG0000132639; Homo sapiens
HGNC; HGNC:11132; SNAP25. 1KIL; X-ray; C=11-80, D=141-203. 1KTG; X-ray; B=146-204. P60880; 7-83, 131-204. EMBL; L19760; AAC37545.1; -; mRNA. EMBL; L19761; AAC37546.1; -; mRNA. EMBL; D21267; BAA22370.1; -; mRNA. IsoId=P60880-2, P13795-2; Name=SNAP-25b; IsoId=P60880-1, P13795-1; InterPro; IPR000928; SNAP-25 InterPro; IPR000727; T_SNARE and mouse cDNA sequences." Sequence=Displayed; HIX0015639; -. 153735; 153735. 167823; 167823. Name=SNAP-25a;

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                                                                                                                                                                                                                                                                                                          Phosphothreonine (By similarity).
Phosphoserine (By similarity).
ERIEEGADQINKDMKEAEKNLTDLGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP25 MACMU STANDARD; PRT; 206 AA.

P60877; P17955; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
01-QNA-1990 (Rel. 13, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
113-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 Kba protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gimilarity).
SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 SUBUNIT: Part of the SNARE core complex with TRIM9, RIM81, SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with STX1A and VAMP8 (By similarity).
STX1A and VAMP8 (By similarity).
SIMILARITY: Belongs to the SNAP-25 family.
SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                         GMNHINODMKEAEKNLKDLGKCCGLFI (in isoform SNAP-25a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Hippocampus;
Jensen M.J., Smith L.A.;
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: t-SNARE involved in the molecular regulation of
neurorizansmitter release. May play an important role in the
synaptic function of specific neuronal systems. Associates with
proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SMART; SM00397; t_SNARE; 2.
SMART; ENSO192; T_SNARE; 2.
30-structure; Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat; Synaptosome.
DOWAIN
19 81
t_SNARE coiled-coil homology 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 79; DB 1; Length 206; 100.0%; Pred. No. 1.8e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23315 MW; FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                               Cleavage (by BONT/E)
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                                                                                                                                                                                                                                                       Cys-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               $\text{SNP25}$ MOUSE STANDARD; PRT; 206 AA. $\text{P60879}$; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45; $\text{O1-JAN-1990}$ (Rel. 13, Created) $\text{Carted}$; $\text{O1-JAN-1990}$ (Rel. 13, Last sequence update) $\text{13-SEP-2005}$ (Rel. 48, Last annotation update) $\text{SNPAPCSOSMA1-associated protein 25}$ (Synaptosomal-associated brotein 25 (SNAP-25) (Synaptosomal-associated brotein) (SUP). $\text{Name-Snap25}$; Synonyms-Snap; $\text{Mus musculus}$ (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M., Bloom F.E., Wilson M.C.;
"The identification of a novel synaptosomal-associated protein, SNAP-25, differentially expressed by neuronal subpopulations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          Cya-rich.
Cleavage (by BONT/E) (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
PBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21363810; PubMed=11471062; DOI=10.1007/800335-001-1001-x; Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J., Beeson M., Gordon L., Bernett B., Johnson T.E., Sikela J.M.; High-throughput sequence identification of gene coding variants within alcohol-related QILB."; Mamm. Genome 12:657-663(2001).
                                                                                                                                                                                                                                                                                        .;
0
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SWART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/c;
MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
                                                                                                          t-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                   Score 79; DB 1; Length 206;
Pred. No. 1.8e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25B).
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                                                                                                                                                                                                                   23315 MW;
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                                                                                                                                                                                                                                                                   Local Similarity 100.
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140 2
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180 1
138 1
187 1
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                                                                                         Synaptosome.
DOMAIN
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SEQUENCE
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Ravai T., Reed J.C., Reed D.J., Raid J.D., Ramachandran S.,
Ravai T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
A Sultana R., Takenaka Y., Taylor M.S., Teaedale R.D., Tomita M.,
A Sultana R., Takenaka Y., Taylor M.S., Teaedale R.D., Tomita M.,
A Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
A Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
A Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayateu N.,
A Niraki T., Waki K., Kawai J., Aizawa M., Sakazume N., Sato K.,
A Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
A Niyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
A Yashino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayachizaki Y.;
A Malysis C. the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3; Hepp R., Cabaniols J.P., Roche P.A.; "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion. SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 SNAP25BP and HGS. Binds CPLX1. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 532:52-56(2002).
-!- FUNCTION: t-SNARE involved in the molecular regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10195194; DOI=10.1038/5673;
Ilardi J.M., Mochida S., Sheng Z.-H.;
"Snapin: a SNARE-associated protein implicated in synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
3L/6; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Sequence=VSP_010019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nat. Neurosci. 2:119-124(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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-i- PTM: Palmitoylated (By similarity).
-i- SIMILARITY: Belongs to the SNAP-25 family.
-i- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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Search completed: April 3, 2006, 15:46:25 Job time: 83.4954 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 3, 2006, 15:30:10 ; Search time 8.66055 Seconds (without alignments) 177.756 Million cell updates/sec

US-09-942-098-29 79

1 SNKTRIDEANQRATKM 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		protein	synapse protein SN	synaptosomal-assoc		nerve terminal pro	synaptosomal-assoc	synapse protein -	SNARE protein 23 -		н	hypothetical prote	w			hypothetical prote	lipoprotein [impor			hypothetical prote		hypothetical prote		_	d T			ical prot	suitatas	probable sulfatase
	ΩI		I50481	I50480	A37861	153735	167823	A33623	I50552	JC5512	JC5297	JC5296	T26553	E81436	850562	T29999	T32127	G90551	F96966	T09481	T20653	G88545	831132	A33854	A47483	AB1996	S68784	T26205	1991	6498	B85858
	BB	;	7	N	7	~	N	~	~	~	~	~	7	~	7	~	~	N	N	7	~	~	7	7	~	~	~	~	7	Н	7
	Query Match Length		203	204	206	206	206	206	210	210	158	211	234	401	420	2288	393	642	575	1314	243	918	943	83	217	219	294	_	465	æ	8
æ	Query		100.0	100.0	100.0	100.0	100.0	100.0	77.2	60.8	55.7	55.7	53.2	53.2	53.2	53.2	51.9	51.9	50.6	50.0	49.4	48.7	48.7	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1
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	Result No.		-	8	e	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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H91013 T32269	H89864 C96637	118824 873710	A35312	S64386 A64085	JU0271	B69863	A32579	T16613	\$60851
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586 643	1272	290	4 90	4 9 4 5 5 2	630	738	1239	2427	9
48.1	48.1	4 4 6 6 6 6 8 8 8	46.8	46.8	46.8	46.8	46.8	46.8	45.6
38	388	37	37	37	37	37	37	37	36
30	288	3 5 5 5	37	38	0.4	4 T 4 Z	43	44	45

ALIGNMENTS

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synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Species: L3-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50481
R;Risinger, C; Larhiammar, D.
R;Risinger, C; Larhiammar, D.
R;Accession: SNAP-25 in the tetraploid goldfish.
A;Accession: I50481
A;Accession: I50481
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-203 RIS>
A;Residues: 1-203 RIS>
A;Residues: 1-203 RIS>
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 203;
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RESULT 1
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0; Indels y Match 100.0%; Score 79; DB 2; I Local Similarity 100.0%; Pred. No. 2.3e-06; as 16; Conservative 0; Mismatches 0; Best Loc Matches

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Gaps

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SNKTRIDEANQRATKM 199 1 SNKTRIDEANORATKM 16 184 엄 ઠે

RESULT 2

synapse protein SNAP-25 - goldfish synapse protein SNAP-25 - goldfish (c;Species: Carassius auratus (goldfish) (c;Species: 13-Sep-1996 #text_change 09-Jul-2004 (c;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 (c;Date: 13-Sep-1996 #sequence_revision 150480 (c;Accession: 120480 (c;Accession: 12

Gaps ö Length 204; Score 79; DB 2; Length 20 Pred. No. 2.3e-06; Mismatches 0; Indels ö 100.0%; 16 1 SNKTRIDEANORATKM Conservative Local Similarity tes 16; Conserva Query Match Best Loca Matches à

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Mon Apr

Best Loca Matches

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synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; V
J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differer
A;Reference number: A33623; MuID:90078337; PMID:2592413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synapse protein - marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150552
C;Accession: 150552
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shc A;Reference number: A49513; WID:94043281; PMID:8226991
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Okaz
Biochem. Biophys. Res. Commun. 244, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Muncl8c.
A;Reference number: JC5512; MUID:97312558; PMID:9168999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: mm.
A,Residues: 1-206 <0XLs
A,Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:G200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFE; GB:L22020; NID:g431296; PIDN:
                                                                                                                                                  Gaps
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                                                                                        Length 206;
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100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                        Score 79; DB 2;
Pred. No. 2.3e-06;
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A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
                                                                   100.0%; 5cc...
100.0%; Pred. No. 4...
0; Mismatches
A, Cross-references: GDB:355671; OMIM:600322
A, Map position: 20p11.2-20p11.2
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                                                                                                                                                                                                             1 SNKTRIDEANORATKM 16
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                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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Matches
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R;Bark, I.C.; Wilson, M.C.
A;Green 139, 291-292, 1994
A;Green 159, 1994
A;Artle: Human cDNA clones encoding two different isoforms of the nerve terminal protein A;Reference number: I53735, MUID:94156217, PMID:8112622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein A,Reference number: 153735; MUID:94156217; PMID:8112622 A,Accession: 167823
                                                                                                                                                                                                                C;Accession: A37861
R;Catesicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid
A;Reference number: A37861; MUID:91126080; PMID:1992470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Modecule type: mRNA
A;Residues: 1-206 «FESS»
A;Cross-references: UNIPROT:P60880; UNIPARC:UP1000002B3DD; GB:L19760; NID:g307425; PIDN:
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A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:P60878; UNIPARC:UP10000001103; GB:M57957; NID:g212673; PIDN:
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 167923
R;Bark, 1.C.; Wilson, M.C.
Gene 139, 291-292, 1994
                                                                                                                          synaptosomal-associated 25% protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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Pred. No. 2.3e-06;
Mismatches 0; Indels
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A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
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Genetics:

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hypothetical protein YER059w - yeast (Saccharomyces cerevisiae)
C;Species: Sacharomyces cerevisiae
C;Species: Sacharomyces cerevisiae
C;Date: 28 **May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: S50562
Submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.
A;Accession: S50427
A;Accession: S50626
A;Molecule type: DNA
A;Residues: 1-420 **CDE>
A;Accession: Company Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liansemembrane transport protein Cj0182 [imported] - Campylobacter jejuni (strain NCTC 111]
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
R;Parkhill, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;File: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
R;Gardner, A.
submitted to the EMBL Data Library, January 1998
A;Reference number: 220231
A;Accession: T2653
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: UNIPROT:062414; UNIPARC:UPI0000164256; EMBL:AL021479; PIDN:CAA16322.1
A;Experimental source: clone Y22F5A
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A;Residues: UNIPROT:Q9PIU7; UNIPARC:UPI00000C207C; GB:AL139074; GB:AL11168; NID:
A;Experimental source: serotype O2, strain NCTC 11168
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C;Superfamily: probable inner membrane transport protein bacA
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Pred. No. 14;
1; Mismatches
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Local Similarity 43.8%; Pred. No. 8.1;
les 7; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 5
A,Introns: 51/3; 82/1; 165/2; 213/3
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les 9; Conservat
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A, Status: preliminary
A, Molecule type: DNA
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A;Residues: 1-211 : «MOL»
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI000000A2C; GB:Y09567; NID:91924941; PIDN
C;Coment: This protein is involved in regulating exocytosis in human neutrophils, a cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:000161; UNIPARC:UP1000002B3DC; GB:Y09568; NID:g1924943; PIDN
A;Experimental source: neutrophils
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cen
                                                                           A;Gross-references: UNIPROT:009044; UNIPARC:UPI0000022B5C; DDBJ:AB000822; NID:92189950; C;Comment: This protein is involved in the insulin-induced translocation of vesicles con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: ÚC5296
R;Mollinedo, F.; Lazo, P.A.
R;Mollinedo, F.; Lazo, P.A.
R;Mollinedo, B.; Lazo, P.A.
R;Mollinedo, B.; Lazo, P.A.
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23
A;Reference number: UC5296; MUID:97224437; PMID:9070898
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vesicle-membrane fusion protein SNAP-23A - human
C;Species: Homo sapiens (man)
C;Date: 02-May_1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 211;
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                                                                                                                                                                               Length 210;
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Pred. No. 3.2;
3; Mismatches
                                                                                                                                                                               Query Match 60.8%; Score 48; DB 2; Best Local Similarity 62.5%; Pred. No. 0.64; Matches 10; Conservative 2; Mismatches
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140 TNRDRIDIANARAKKL 155
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192 TNKNRIDIANTRAKKL 207
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Best Local Similarity 56.2%;
Matches 9; Conservative
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A; Residues: 1-158 <MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                 A;Molecule type: mRNA
A;Residues: 1-210 <ARA>
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Best Local S
Matches 9
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hypothetical protein ZC8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T2999
R;Atrealle, P.; Bradshaw, H.
R;Atrealle, P.; Bradshaw, H.
R;Abescription: T4999
A;Accession: T2999
A;Accession: T2999
A;Accession: T2999
A;Accession: T2999
A;Accession: T2989
A;Accession: T2989
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A;Accession: T2989
A;Accession: T2989
A;Accession: T2989
A;Accession: E2989
A;Accession: E2989
A;Accession: E2989
A;Accession: Bristol NIPROT:Q23081; UNIPARC:UPI000017BCE7; EMBL:U64862; PIDN:AAB52624.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:ZC8.4
A;Map position: X
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:016766; UNIPARC:UP100001642E9; EMBL:AF016686; PIDN:AAB66239.
A;Experimental source: strain Bristol N2; clone R07C3
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                                                   Gaps
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A;Introns: 20/1; 350/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C32B5.10
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51.9%; Score 41; DB 2; Length 393;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                   3; Indels
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A;Molecule type: DNA
A;Residues: 1-393 <LAM>
Pred. No. 15; 5; Mismatches
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Job time : 10.6606 secs
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97 AEKMRIKEENEKITKM 112
Best Local Similarity 50.0%;
Matches 8; Conservative
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A;Gene: CESP:R07C3.10
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April 3, 2006, 15:27:08 ; Search time 82.055 Seconds (without alignments) 85.675 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* geneseqp20048:* A_Geneseq_21:* 1:_genesegp1980 Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay44069 Human SNA	Aae36674 Human SNA	Abw01730 Human SNA	Adm97045 Botulinum	Botuli	Aeal4919 Human SNA	Human		Human	Human	Human	Abw01732 Human SNA		Adm97046 Botulinum	Adm97062 Botulinum	Adm97047 Botulinum	Aeal4921 Human SNA	Aea14920 Human SNA	Aae36677 Human SNA	Abw01733 Human SNA	Adm97048 Botulinum	Human	Aab15586 Human SNA	Adp13171 SNAP 25 p
SUMMARIES	ID	AAY44069	AAE36674	ABW01730	ADM97045	ADM97061	AEA14919	AAY44057	AAY44021	ABG69065	AAE36675	AAE36676	ABW01732	ABW01731	ADM97046	ADM97062	ADM97047	AEA14921	AEA14920	AAE36677	ABW01733	ADM97048	AEA14922	AAB15586	ADP13171
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AAW30100 ABW01798 AAE36734	ABWU1/90 AAE36733 ABW01789 AAE36735	AAW30099 AAE36682 AAE36683	AAE36678 ABW01739 ABW01734 ABW01738	ADM97053 ADM97053 AEA14927 AEA14923 AEA14928
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25 27 27	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1 W W W 4 W 4 W	337 337 398	4 4 4 4 4 0 11 6 4 4 3

ALIGNMENTS

Enzymatic assay, quantitation, type A botulinum neurotoxin, proteolysis, fluorescamine, detection, human, synaptosomal protein, SNAP25; Human SNAP25 (amino acids 187-203) analogue [1-16]. AAY44069 standard; peptide; 16 AA. (first entry) 18-JAN-2000 AAY44069; AAY44069

fluorescamine, detection hydrolysis, amino group. Homo sapiens JS5965699-A. 12-OCT-1999.

96US-00743894. 96US-00743894. Schmidt JJ; (USSA) US SEC OF ARMY. 06-NOV-1996; 06-NOV-1996; Bostian KA, Quantitation of type A botulinum toxin. Disclosure; Col 13-14; 28pp; English.

WPI; 1999-579939/49.

The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, minno acids 187-203 of hugarolysis of the peptide is initiated, then stopping hydrolysis of the peptide is unitiated, then stopping hydrolysis of the peptide is unitiated, then stopping hydrolysis of the peptide is contained with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin amount of label produced from a known concentration of toxin measured

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a C BONT A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions. Natural targets of clostridium certain intervenes between the donor fluorophore and acceptor and under the appropriate conditions. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin, to follow activity during production and purification of clostridial toxin and cosmetics. The present sequence is human solved to supple the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                      Human, clostridium toxin, protease activity, botulinum toxin, BoNT, TeNT,
tetanus toxin, VAMP, synaptobrevin, SNAP-25, syntaxin, pharmaceutical;
under similar conditions. The method is useful for the quantitation of
                                                                                                Gaps
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                                                                   Length 16;
                                                                                              0; Indels
                                                                   Score 79; DB 2; I
Pred. No. 4.5e-07;
                                                                                                0; Mismatches
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                                                                                                                                                                                                                         AAE36674 standard; peptide; 16 AA.
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                                                                   100.0%;
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                                                                                                                                          SNKTRIDEANORATKM 16
                                                                                                                          1 SNKTRIDEANQRATKM 16
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                                                                                                                                                                                                                                                                                (first entry
                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                          Human SNAP-25 peptide #5
             type A botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-290198/28.
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003020948-A2
                                          Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steward LE,
                                                                                                                                                                                                                                                                                                                                                                   cosmetic.
                                                                                                                                                                                                                                                      AAE36674;
                                                                                                Matches
                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                             AAE3667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
                                                                                                                                                                                                                                                                                                                                                                                          Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                              Gaps
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ch 100.0%; Score 79; DB 6; Length 16; 1 Similarity 100.0%; Pred. No. 4.5e-07; 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 79; DB 7; Length 16; 100.0%; Pred. No. 4.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulinum toxin substrate recognition sequence #30.
                                                                                                                                                                                                                                                                                                                                                    Human SNAP-25 BoNT/A recognition peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM97045 standard; peptide; 16 AA.
                                                                                                                                                                                                                                 ABW01730 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 10; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                        1 SNKTRIDEANQRATKM 16
                                                                                                                            1 SNKTRIDEANORATKM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001US-00942098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SNKTRIDEANQRATKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEWARD L E.
FERNANDEZ-SALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-829791/77.
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AOKI/) AOKI K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003143651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                               12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2003
                                                                                                                                                                                                                                                                         ABW01730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM97045;
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(FERN/)
                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                           Best Loc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                         RESULT 3
ABW01730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM97045
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clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food
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                                                                                                                                               energy transfer of contacted cell
                                                      04-SEP-2003; 2003WO-US028092.
                                                                                                                                                                                                                                                                                                                                                                                          1 SNKTRIDEANORATKM 16
                                                                                                                                                                                                                                                                                                                                                                                                  SNKTRIDEANQRATKM 16
                                                                    27-SEP-2002; 2002US-00261161
                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                  (ALLR ) ALLERGAN INC
                                                                                                             WPI; 2004-340456/31
                                                                                                Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                    toxin substrate
                             WO2004029576-A2
                                                                                                                                                                                                                                                                                                                                                 Sequence 16 AA;
               Homo sapiens
                                          08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM97061;
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1D ADM9

XX AC ADM9

XX DT 01-1

XX DE BOT1

XX C108

XX Synt
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The invention relates to a method of determining (MI) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (R), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore colostridial toxin recognition sequence with cleavage site intervening between (P) and (A), where under appropriate conditions resonance clostridial toxin recognition sequence with cleavage site intervening clostrophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in contacted cell relative to a control cell, where a difference in cresonance energy transfer of the contacted cell as compared to the contacted cell is indicative of clostridial toxin activity. (MI) is useful control cell is indicative of clostridial toxin activity. (MI) is useful contacted clostridial toxin activity, where the sample is a crude cell is about a contact of clostridial toxin activity, where the sample is a crude control cell is indicative a binding a cellular uptake of the toxin, cranslocation into the cell cytosol and protease activity. In the method control cell cytosol and protease activity. In the method control cell cytosol and protease activity. BonT/G selected from a BonT/A, BoNT/B, BONT/E, BONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human SNAP-25 substrate BoNT/A recognition sequence, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 8; Length 16; 100.0%; Pred. No. 4.5e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 67; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEA14919 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          energy transfer of contacted cell
                                                                                                                                                                                                                                                                                                                                                                   Steward LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                04-SEP-2003; 2003WO-US028092.
                                                                                                                                                                                                                                27-SEP-2002; 2002US-00261161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNKTRIDEANORATKM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNKTRIDEANORATKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   PI; 2004-340456/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin substrate.
                            WO2004029576-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2005
                                                                                            08-APR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEA14919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of determining (MI) clostridial toxin activity, comprising contacting cell with sample comprising clostridial coxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore concertidial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance clostrions and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in contacted cell relative to a control cell, where a difference in cresonance energy transfer of the contacted cell is indicative of clostridial toxin activity. (MI) is useful control cell is indicative of clostridial toxin activity. Where the sample is a crude cell relative clostridial toxin activity, where the sample is a crude cell relations such as binding a cellular upgate of the toxin crudices the need for animal toxicity studies and serves to analyze reduces the need for animal toxicity studies and serves to analyze control into the cell cyclosol and protease activity. In the method MI, the clostridial toxin substrate is a botulinum toxin substrate comprising a BoNT/A, BONT/E, BON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 51; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aoki KR
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Gaps

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29.

Neurotoxin; fluorescence; SNAP-25; botulinum toxin.

JS2005100973-A1

clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.

Synthetic

Botulinum toxin substrate recognition sequence #46.

01-JUL-2004 (first entry)

Homo sapiens.

sample with and second

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The present invention relates to a method for determining protease activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT) and tetanus neurotoxin (TaNT). The method involves treating with a sample, in solution phase under conditions sultable for clostridial toxin protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, syntaxin) comprising fluorescent protein, first partner of affinity couple and clostridial toxin recognition sequence comprising cleavage site; contacting treated sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated sample. The present sequence is the human SNAP-25 substrate BoNT/A (botulinum neurotoxin serotype A) recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic assay, quantitation, type A botulinum neurotoxin, proteolysis;
fluorescamine, detection, human, synaptosomal protein, SNAP25;
                                                                                                                                                                  Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 79; DB 9; I
Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human SNAP25 (amino acids 187-203) analogue #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 29; 97pp; English.
                                                                                                               Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY44057 standard; peptide; 17 AA.
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                            13-AUG-2004; 2004US-00917844.
                                                        28-AUG-2001; 2001US-00942098
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                                                                                    (ALLR ) ALLERGAN SALES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                               Gilmore MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydrolysis; amino group
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                                                                                                                                           WPI; 2005-365632/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 16; Conserv
                                                                                                                                                                                                                  treated sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1996;
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 12-MAY-2005
                                                                                                                Steward LE,
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                                                                    The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolyric activity of botulinum neurotoxin, by determining the proteolyric activity of botulinum hear span and fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNRP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-144076) of the SNRP25 peptide (comprises adding an analogue (e.g. human SNRP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. The method comprises adding an analogue (e.g. AAY44022-Y44076) of this peptide (which represents amino acids 187-203 of the human synaptosomal protein SNAP25) to a sample contening the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the different time points; and measuring the amount of hydrolysis at each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic assay, quantitation, type A botulinum neurotoxin, proteolysis;
fluorescamine; detection, human, synaptosomal protein, SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 79; DB 2; Length 17; 100.0%; Pred. No. 4.9e-07; ive 0; Mismatches 0; Indels
Quantitation of type A botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quantitation of type A botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acids 187-203 of human SNAP25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY44021 standard; peptide; 17 AA.
                                        Disclosure; Col 9; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 4; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bostian KA, Schmidt JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nydrolysis; amino group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                   type A botulinum toxin
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
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neurotoxin light chain (BoWT LC) serotype A, where the DNA has a sequence that is expressible in a host organism other than Clostridium, or has a total A+T content that is less than about 70% The BOWT LC protein is useful in vaccination against botulism, for eliciting protective immunity in a mammal, for treating dystonias, spasticity, pain, ocular motility, facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles, control autonomic nerve function or tiptoe-walking due to stiff muscles common in children with cerebral palsy. The sequences are also useful for screening for botulinum neurotoxin inhibitors. This sequence represents a human polypeptide C-terminal fragment, used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain; spasticity; ocular motility; facial dyskinesia; stiff-person syndrome; bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human; commetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant; lower motor neuron hyperactivity; autonomic nerve function; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid molecule encoding botulinum neurotoxin light chain serotype A, useful for producing the neurotoxin for vaccination against botulism, comprises sequence expressible in host other than Clostridium
time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a nucleic acid molecule encoding a botulinum
                                                                                                                                                                                                                                                                                                                               Length 17;
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                                                                                                                                                                                                                                                                                                                                      100.0%; Score 79; DB 2; L 100.0%; Pred. No. 4.9e-07;
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20-JUL-2001; 2001US-00910186.
09-AUG-2001; 2001US-0311966P.
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                             type A botulinum toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-575192/61.
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Matches 16; Conserv
                                                                                                                                                                                                                                                                Sequence 17 AA;
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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance appetrum overlapping the emission spectrum of the donor fluorophore and abor A or BoNT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lyamate, raw, cooked or processed foods, beverages, animal feed, animal amminer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human, clostridium toxin, protease activity, botulinum toxin, BoNT; TeNT; tetanus toxin, VAMP; synaptobrevin, SNAP-25; syntaxin, pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is human SNAP-25 peptide used in the invention
                                                                                      Gaps
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                                                Length 17;
                                                                                      Indels
                                                    100.0%; Score 79; DB 5;
100.0%; Pred. No. 4.9e-07;
                                                                                          Mismatches
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                                                                  Pred No.
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                                                                                                                                                                                                                                                                    AAE36675 standard; peptide; 17 AA.
                                                          100.0%;
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                                                                                                                                1 SNKTRIDEANORATKM 16
                                                                                                                                                                SNKTRIDEANORATKM 16
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Human SNAP-25 peptide #6
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                                                      Query Match
Best Local Similarity
Matches 16; Conserv
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                  Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cosmetic.
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                                                                                                                                                                                                                              RESULT 10
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Score 79; DB 6; Length 17; Pred. No. 4.9e-07;

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Query Match Best Local Similarity

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ABW01732 standard; peptide; 17 AA.
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(FERN) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
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                                                                              ABW01732;
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                                                                                                                                                                                                                           human
RESULT 12
ABW01732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a CBOMT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is human SNAP-25 peptide used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                       Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
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                                                                                                                                            AAE36676 standard; peptide; 17 AA.
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                               SNKTRIDEANORATKM
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                                                                                                                                                                                                                                                                  Human SNAP-25 peptide #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALLR ) ALLERGAN INC
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clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining clostridial toxin protease activity, by treating sample with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
                                                                                       Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
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                                            Human SNAP-25 BoNT/A recognition peptide #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steward LE, Fernandez-Salas E,
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(first entry)
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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                       The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanns toxins. The present sequence is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin; fluorophore; clostridial toxin product; BOTOX; food.
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                                                                                                                                                                                                                                                                                                                                                            Score 79; DB 7; Length 17;
Pred. No. 4.9e-07;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulinum toxin substrate recognition sequence #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 52; 188pp; English.
                                                                                                                           Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM97046 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            energy transfer of contacted cell
                                                                                                                                                                                                                                Disclosure; Page 10; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steward LE,
                                                                                                                           Fernandez-Salas E,
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                                                                                                                                                                                                                                                                                                                                                                100.0%;
                        28-AUG-2001; 2001US-00942098.
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                                                28-AUG-2001; 2001US-00942098
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                          STEWARD L E.
FERNANDEZ-SALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-340456/31.
                                                                                                                                                   WPI; 2003-829791/77
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                                                                                                 AOKI K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004029576-A2
                                                                                                                                                                                                                                                                                                                                       Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clostridial
                                                                                                                            Steward LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-2004
31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM97046;
                                                                                      (FERN/)
(AOKI/)
                                                                          (STEW/)
                                                                                                                                                                                                                                                                                                                peptide
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The invention relates to a method of determining (M1) clostridial toxin

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Gaps

The invention relates to a method of determining (MI) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food Gaps ö 100.0%; Score 79; DB 8; Length 17; 100.0%; Pred. No. 4.9e-07; Live 0; Mismatches 0; Indels Botulinum toxin substrate recognition sequence #47. Disclosure, SEQ ID NO 68; 188pp; English. Aoki KR energy transfer of contacted cell ADM97062 standard; peptide; 17 AA Steward LE, 04-SEP-2003; 2003WO-US028092. 27-SEP-2002; 2002US-00261161 1 SNKTRIDEANQRATKM 16 SNKTRIDEANQRATKM 16 01-JUL-2004 (first entry) Local Similarity 100. nes 16; Conservative (ALLR) ALLERGAN INC Fernandez-Salas E, WPI; 2004-340456/31 402004029576-A2 toxin substrate Sequence 17 AA; 08-APR-2004 Synthetic ADM97062; Query Match Matches RESULT 15 ADM97062 셤 8

contridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in control cell is indicative of the contacted cell as compared to the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (MI) is useful for determining clostridial toxin formulated clostridial toxin cell lysate, isolated clostridial toxin, formulated clostridial toxin cell lysate, both of control is an automorated high-throughput assay. (MI) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, the clostridial toxin substrate is a botulinum toxin substrate selected from a BonT/A, BoNT/B, BONT/C, BONT/E, BONT/E, BONT/F, BONT/F, BONT/E, BONT/E, BONT/F, BONT/F, BONT/E, BONT/E, BONT/C, BONT/E, BONT/F, BONT/F, BONT/F, BONT/F, BONT/E, Cot In substrate comprising a botulinum toxin sequence corresponds to a recognition sequence for a botulinum toxin used as the clostridial \$

Sequence 17 AA;

ö Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels

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Search completed: April 3, 2006, 15:36:56 Job time : 82.2217 secs

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RESULT 2
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Sequence 33, Appl
Sequence 33, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
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235.925 Million cell updates/sec
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                                                                            April 3, 2006, 15:23:07 ; Search time 2.19355 Seconds
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1: /SIDS5/ptodata/1/pubpaa/US06 NEW PUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US06 NEW-PUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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7: /SIDS5/ptodata/1/pubpaa/US10 NEW PUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10 NEW PUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US10 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-948-097-33
US-10-948-097-35
US-10-947-071-35
US-10-947-071-41
US-10-947-071-41
US-10-948-097-36
US-10-948-097-36
US-10-948-097-41
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US-10-948-097-1
US-10-948-097-1
US-10-948-097-2
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                                                                                                                                                                                                                          180808 seqs, 30441898 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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26 79 95.2 16 6 US-10-948-097-32 Sequence 32, Appl 28 79 95.2 17 6 US-10-947-071-53 Sequence 34, Appl 28 79 95.2 17 6 US-10-947-071-55 Sequence 53, Appl 30 79 95.2 17 6 US-10-947-071-55 Sequence 53, Appl 31 79 95.2 17 6 US-10-948-097-34 Sequence 54, Appl 32 79 95.2 17 6 US-10-948-097-55 Sequence 54, Appl 32 79 95.2 17 6 US-10-948-097-55 Sequence 57, Appl 34 79 95.2 17 6 US-10-948-097-55 Sequence 57, Appl 36 78 94.0 17 6 US-10-948-097-55 Sequence 57, Appl 36 78 94.0 17 6 US-10-948-097-56 Sequence 56, Appl 36 78 94.0 17 6 US-10-948-097-56 Sequence 54, Appl 37 79 94.0 17 6 US-10-948-097-58 Sequence 54, Appl 39 78 94.0 17 6 US-10-948-097-58 Sequence 54, Appl 40 77 92.8 17 6 US-10-948-097-58 Sequence 56, Appl 41 77 92.8 17 6 US-10-948-097-58 Sequence 57, Appl 42 77 92.8 17 6 US-10-948-097-58 Sequence 50, Appl 42 77 92.8 17 6 US-10-948-097-58 Sequence 51, Appl 44 77 92.8 17 6 US-10-947-071-50 Sequence 51, Appl 44 77 92.8 17 6 US-10-947-071-50 Sequence 52, Appl 44 77 92.8 17 6 US-10-947-071-50 Sequence 52, Appl 44 77 92.8 17 6 US-10-947-071-50 Sequence 52, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 52, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 52, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 52, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 52, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 52, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77 92.8 17 6 US-10-947-071-51 Sequence 56, Appl 54 77
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ALIGNMENTS

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Sequence 31, Application US/10980346B

Sequence 31, Application US/20060024763A1

Publication No. US20060024763A1

GENERAL INFORMATION:

APPLICANT: Los Alamos National Laboratory

APPLICANT: Schmidt, Jurgen G., et al.

TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation

TITLE OF INVENTION: of Botulinum Neurotoxins

FILE REFREBRES: 5-102,313

CURRENT FILING DATE: 2004-11-03

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn version 3.2

SEQ ID NO 37

LENGTH: 17
Squence 6. Application US/10980346B

Sguence 6. Application US/10980346B

Schult and No. US20060024763A1

GRNERAL INFORMATION:

SAPPLICANT: Los Alamos National Laboratory

APPLICANT: Schmidt, Jurgen G, et al.

TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation

TITLE OF INVENTION: Of Botulinum Neurotoxins

FILE REPERENCE: S-102,313

CURRENT APPLICATION NUMBER: US/10/980,346B

CURRENT PILING DATE: 2004-11-03

NUMBER OF SEQ ID NOS: 55

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
OTHER INFORMATION: Neurotoxin (BoNT)
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 17; Conservative
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| Sequence 35, Application US/10947071
| Publication No. US20060063221A1
| Publication No. US20060063221A1
| GENREAL INFORMATION:
| APPLICANT: Williams, Dudley J. |
| APPLICANT: Werhagen, Marcella |
| APPLICANT: Overhagen, Marcella |
| APPLICANT: APPLICANT: Por Determining Clostridial Toxin Activity |
| TITLE OF INVENTION: Lanthanide-Based Substrates and Methods |
| TITLE OF INVENTION: Lanthanide |
| TITLE OF INVENTION: For Determining Clostridial Toxin Activity |
| FILE REFERENCE: 66872-043 |
| CURRENT APPLICATION NUMBER: US/10/947,071 |
| CURRENT FILING DATE: 2004-09-21 |
| NUMBER OF SEQ ID NOS: 101 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| EMOUNT HOUSE |
| LEWING HOU
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Sequence 35, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Gilmore, Marcella

APPLICANT: AONI, Kei Roger

ITTLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REPERENCE: 66872-440

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOPTWARE: PARKEDQ for Windows Version 4.0

FIRMOREM OF SEQ ID NOS: 96

SEQ ID NOS: 58

FIRMOREM OF SEQ ID NOS: 96

FIRMOREM OF SEQ ID NOS: 96
                                                                 Query Match
100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0
----hes 17; Conservative
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; ORGANISM: Homo sapiens
US-10-947-071-35
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ORGANISM: Homo sapiens
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                                                                                                                   OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum OTHER INFORMATION: Neurotoxin (BoNT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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| Sequence 33, Application No. US20060063221A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Dudley J. APPLICANT: Glimore, Marcella
| APPLICANT: Steward, Lance
| APPLICANT: Steward, Lance
| APPLICANT: Verhagen, Marce
| APPLICANT: Verhagen, Marce
| APPLICANT: Aoki, Kei Roger
| TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
| TITLE OF INVENTION: Lanthanide Clostridial Toxin Activity
| FILE REFERENCE: 66872-043
| TITLE OF INVENTION: Lanthanide Clostridial Toxin Activity
| FILE REFERENCE: 66872-043
| CURRENT APPLICATION NUMBER: US/10/947,071
| CURRENT PILLING DATE: 2004-09-21
| NUMBER OF SEQ ID NOS: 101
| SEQ ID NO 33
| LEMOTH: 17
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Sequence 33, Application US/10948097

Publication No. US20060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Defermining Clostridial Toxin Activity

FILLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REPERENCE: 66872-040

CURRENT FILING DATE: 2004-09-22

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 33

LENGTH: 17

TOTAL DENGTH: 17

TOTAL DENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 83; DB 6; Length 17; Best Local Similarity 100.0%; Pred. No. 8.1e-09; Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                             FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (1)...(17)

OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SNKTRIDEANORATKML 17
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                                     ORGANISM: Artificial Sequence PEATURE:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gaps

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APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marce
APPLICANT: Verhagen, Marce
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-948-097-36

US-10-948-097-36

is Sequence 36, Application US/10948097

; Publication No. US2006005322A1

; GENERAL INFORMATION:

is APPLICANT: Verhagen, Marc

; APPLICANT: Gilmore, Marcella

; APPLICANT: Steward, Lance

; APPLICANT: Acki, Kei Roger

; TITLE OF INVENTION: Determining Clostridial Toxin Activity

; TITLE OF INVENTION: Determining Clostridial Toxin Activity

; TITLE OF INVENTION: Determining Clostridial Toxin Activity

; CURRENT FILING DATE: 2004-09-22

; CURRENT FILING DATE: 2004-09-22

; SEQ ID NO 36

; SEQ ID NO 36

; LENGHH: 33

**COFFMARE: FASTEED for Windows Version 4.0

; EBNGHH: 33
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| Sequence 40, Application US/10948097
| Sequence 40, Application US/10948097
| Publication No. US20060063222A1
| GENERAL INFORMATION:
| APPLICANT: Willams, Dudley J.
| APPLICANT: Gilmore, Marcella
| APPLICANT: Gilmore, Marcella
| APPLICANT: Greward, Lance
| APPLICANT: Application Fluorescence Polarization Assays For TITLE OF INVENTION: Fluorescence Polarization Assays For TITLE OF INVENTION: Determining Clostridial Toxin Activity FILE REFERENCE: 66872-040
| CURRENT PAPLICATION NUMBER: US/10/948,097
| CURRENT FILING DATE: 2004-09-22
| NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 83; DB 6; Length 33; 100.0%; Pred. No. 1.8e-08;
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ORGANISM: Mus musculus
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Best Local Similarity
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APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REPERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEO ID NOS: 101
SOFTWARE: Fast-SEO for Windows Version 4.0
                                                                                                                              Sequence 36, Application US/10947071

Sequence 36, Application US/10947071

SEQUENCE No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Acki, Rei Roger

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: Lanthaning Clostridial Toxin Activity

FILE REFERENCE: 66972-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SEQ ID NOS: 101

SEQ ID NOS: 101

TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 83; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-947-071-40
; Sequence 40. Application US/10947071
; Publication No. US20060053221A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Mus musculus US-10-947-071-36
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US-10-947-071-41
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OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Aoki, Kel Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REPERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 6; Length 203; Pred. No. 1.5e-07;
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                                                                                                                                                                        Query Match
100.0%; Score 83; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10948097
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
    APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
    APPLICANT: Gilmore, Marcella
    APPLICANT: Steward, Lance
; APPLICANT: Acki, Kei Roger
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FeatSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining Clostridial Toxin Activity
                            ; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-11-195-098-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 203
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Publication No. US20060063221A1
GENERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
                                                                                                                                                                                                                                                                                                                         96 SNKTRIDEANQRATKML 112
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; ORGANISM: Carassius auratus
US-10-948-097-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Carassius auratus
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Best Local Similarity
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Sequence 11, Application US/11195098
Sequence 11, Application US/11195098
GENERAL INFORMATION:
APPLICANT: Schmidt, James J.
TITLE OF INVENTION: Hourotoxins
FILE REFREENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/11/195,098
CURRENT FILING DATE: 2004-08-02
PRIOR APPLICATION NUMBER: US/10/802,574
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
LENGTH: 116
TTENE PRIOR FILING
TTENE APPLICATION NUMBER: US/10/802,574
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
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JAPPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Marcella
APPLICANT: Glunce, Marcella
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Pluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 33
TYPE: PRT
                                                                                                                                                                                   Length 33;
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Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0;
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40 LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/10948097
Publication No. US20060063222A1
GENERAL INFORMATION:
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US-10-948-097-41
                                                                                                         ; ORGANISM: Carassius auratus
US-10-948-097-40
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Matches 17; Conservative 0; Mismatches 0; Indels

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US-09-942-098-30
Sequence 30, Application US/09942098
Sequence 30, Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
TAPPLICANT: Steward, Lance E.
APPLICANT: Aokl, Kel Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
NUMBER OF SEQ ID NOS: 96
NUMBER FELENCE: PRESECT OF WINDOWS Version 4.0
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; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Acki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Fret Protease Assays
; TITLE OF INVENTION: Fret Protease
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT APPLICATION NUMBER: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
US-10-917-844-37

US-10-917-844-38

US-10-705-854-4

US-10-917-844-112

US-09-952-360B-11

US-09-942-0514-14

US-09-942-098-14

US-09-942-098-14

US-10-261-161-7

US-09-942-024-14

US-09-942-024-12

US-09-942-024-12

US-09-942-098-2

US-09-942-088-2
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       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30
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ORGANISM: Homo sapiens
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           LENGTH: 17
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1. /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

2. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

3. /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
                                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-942-098-30
US-10-011-58-30
US-10-261-161-68
US-10-261-161-68
US-10-942-024-32
US-09-942-024-32
US-10-917-844-32
US-10-917-844-32
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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US-10-917-844-30
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US-10-011-588-2

Sequence 2, Application US/10011588

Publication No. US20020168727A1

GENERAL INFORMATION:
APPLICANT: Smith, Leonard

APPLICANT: Smith, Leonard

TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM

TITLE OF INVENTION: RECOMBINANT LIGHT CHAIN FUSION PROTEINS FOR USE IN

TITLE OF INVENTION: RESPARCH AND LIGHT CHAIN FUSION PROTEINS

TITLE OF INVENTION: RESPARCH AND LIGHT CHAIN FUSION PROTEINS

CURRENT APPLICATION NUMBER: US/10/011,588

CURRENT APPLICATION NUMBER: US/200-03-29

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FALSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 17

TYPE: PRE
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Sequence 52, Application US/10261161

Sequence 52, Application No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT PILICATION NUMBER: US/10/261,161

CURRENT PILICATION NUMBER: US/200-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 52
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Query Match
100.0%; Score 83; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-52
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US-10-917-644-30

Sequence 30, Application US/10917844

Publication No. US20050100973A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Gilmore, Marcella A.
TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
TITLE OF INVENTION: WHERE: US/10/917,844

CURRENT FILING DATE: 2004-08-13

PRIOR FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 113

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFRENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PRATSEQ for Windows Version 4.0
SEQ ID NO 68
LENGTH: 17
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Query Match 100.0%; Score 83; DB 4; Length 17; Best Local Similarity 100.0%; Pred. No. 3.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: synthetic construct
US-10-261-161-68
                                                                                                                                                                                                                                    RESULT 5
US-10-261-161-68
Sequence 68, Application US/10261161
Sequence 68, Application US/10261161
Publication No. US20040072270A1
GENERAL INFORMATION
GENERAL INFORMATION
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ORGANISM: Homo sapiens
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Query Match
Best Local Similarity
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; Sequence 54, Application US/2026161
; Publication No. US2004007227081
; GENERAL INFORMATION:
; APPLICANT: Sermandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial TELLS REFERENCE: P-AR 404
; CURRENT APPLICANTON NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 83; DB 3; Length 18; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
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Sequence 32. Application No. US20030143651A1

GENERAL INPORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Renandez-Salas, Ester
APPLICANT: Roil Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICANTON HOWBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ IN NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 83; DB 3; Length 18; 100.0%; Pred. No. 3.6e-07; tive 0; Mismatches 0; Indels
Sequence 32, Application US/09942024
; Sequence 32, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/F Toxins
; TITLE OF INVENTION: Serotype A/F Toxins
; TITLE OF INVENTION: Serotype A/F Toxins
; CURRENT PFLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NOS: 96
; SEQ ID NOS: 97
; LENGTH: 18
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNKTRIDEANQRATKML 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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US-09-942-098-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-942-024-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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JARLEANT: RENABLY, BEATRICE

TITLE OF INVENTION: USE OF A COMBINATION OF COMPONENTS WITH AN INHIBITORY
TITLE OF INVENTION: USE OF A COMBINATION OF CALCIUM CHANNELS TO PREVENT OR
TITLE OF INVENTION: TREAT WRINKLES AND FINE LINES
TITLE OF INVENTION: TREAT WRINKLES AND FINE LINES
TITLE OF INVENTION: UNMBER: US/10/705,857
CURRENT APPLICATION NUMBER: 00/427,575
PRIOR APPLICATION NUMBER: 60/427,575
PRIOR APPLICATION NUMBER: ER 0214183
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOICE: 3.2
LENGTH: 19
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CURRENT PPLICATION NUMBER: US/10/917,844
CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US 09/942,098
PRIOR FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 83; DB 5; Length 18; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                           100.0%; Score 83; DB 4; Length 18; 100.0%; Pred. No. 3.6e-07; tive 0; Mismatches 0; Indels
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 113
SOFTWARE: PattSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-917-844-32; Application US/10917844; Sequence 32, Application US20050100973A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10705857 Publication No. US20040147443A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SNKTRIDEANQRATKML 18
                                                                                                                                                                                                                                                                                                                                  2 SNKTRIDEANQRATKML 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
The Conservative
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CRGANISM: Homo sapiens
US-10-917-844-32
                                                                                                     TYPE: PRT CORGANISM: Homo sapiens US-10-261-161-54
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OTHER INFORMATION: synthetic peptide
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NAME/KEY: MOD_RES
LOCATION: 100
OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 21
COTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 89, Application US/09942098
; Beduce 89, Application No. US20030143651A1
; GENERAL INFORMATION:
    APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas,
    TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION UNDER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 89
; SEQ ID NO 89
; LENGTH: 21
                                                                   Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Score 83; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Steward, Lance E.
APPLICANT: Fernandea-Salss, Ester
APPLICANT: Acking Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REPERROR: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 21
                                                                   Score 83; DB 4; I Pred. No. 3.8e-07;
                                                                                                            0; Mismatches
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OTHER INFORMATION: at the C-terminal
                                                                                                                                                                                                                                                                                 US-09-942-024-89; Sequence 89, Application US/09942024; Publication No. US20030143650A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNKTRIDEANORATKML 20
                                                               Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative 0
                                                                                                                                                         1 SNKTRIDEANORATKML 17
                                                                                                                                                                                                  3 SNKTRIDEANORATKML 19
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ORGANISM: Artificial Sequence
PEATURE:
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  , OTHER INFORMATION: peptide US-10-705-857-6
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NAME/KEY: MOD_RES

LOCATION: 1

OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES

LOCATION: 21

OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION

LOCATION: (0) ... (0)

OTHER INFORMATION: at the C-terminal
US-09-942-098-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine NAME/KEY: AMIDATION LOCATION: (0)...(0)
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100.0%; Score 83; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         Length 21
                                                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE FastSEQ for Windows Version 4.0
LENGTH: 23
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Sequence 88, Application US/09942098
Sequence 88, Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa=fluorescein-modified lysine NAME/XEY: MOD_RES LOCATION: 23
                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 83; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0;
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OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
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OTHER INFORMATION: at the C-terminal
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ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PESESEG for Windows Version 4.0

SEQ ID NO 88

LENGTH: 23

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
NAME/KEY: MOD_RES

LOCATION: 1

OCCATION: 13

COCATION: 23

LOCATION: AMIDATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION: At the C-terminal
LOCATION: (0)

COCATION: (1)

OTHER INFORMATION: at the C-terminal
US-09-942-098-88

OLOCATION: (1)

SECOND INFORMATION: AMIDATION

LOCATION: (1)

COLEY MATCH

SECOND INFORMATION: AMIDATION

LOCATION: (1)

SECOND INFORMATION: AMIDATION

LOCATION: (1)

SECOND INFORMATION: AMIDATION

LOCATION: (1)

SECOND INFORMATION: AMIDATION

LOCATION: (2)

COLEY MATCH

SECOND INFORMATION: AMIDATION

LOCATION: (3)

SECOND INFORMATION: AMIDATION

LOCATION: (4)

COLEY MATCH

BEST LOCATION: (1)

SECOND INFORMATION: AMIDATION

LOCATION: (2)

SEQ ID 100.00

AMIGNATION

LOCATION: (3)

LOCATION: (4)

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                                                                                                                                        3, 2006, 15:16:44; Search time 4.52419 Seconds (without alignments) 310.660 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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. /Ggn2_6/ptodata/1/iaa/5_COMB.pep:*
. /Cgn2_6/ptodata/1/iaa/6_COMB.pep:*
. /Cgn2_6/ptodata/1/iaa/H_COMB.pep:*
. /Cgn2_6/ptodata/1/iaa/H_COMB.pep:*
. /Cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
. /Cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
. /Cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-743-894B-1
US-08-819-286-9
US-08-819-286-4
US-08-189-286-4
US-08-78-560-10
US-09-534-572-10
US-09-953-560-11
US-09-949-016-05311
US-09-949-016-06311
US-08-733-98F-18
US-08-743-894B-19
US-08-743-894B-32
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US-08-743-894B-50
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                    1 SNKTRIDEANQRATKML 17
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                             score:
                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                                      Title:
Perfect
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Sequence 1, Application US/08743894B

Pacent No. 2955699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Agres J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin frontmember OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MEMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
TION ATTOLEMA
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Sequence 38,
Sequence 3, 1
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US-08-743-894B-24
US-08-743-894B-26
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-34
US-08-743-894B-34
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-45
US-09-962-360B-8
US-09-962-360B-12
US-08-743-894B-35
US-08-743-894B-35
US-08-743-894B-35
US-08-743-894B-38
US-08-743-894B-47
US-08-743-894B-47
US-08-743-894B-48
US-08-743-894B-48
US-08-743-894B-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CILASSIFTCATION: 435
FILING DATE: APPLICATION: APPLICATION DATA:
APPLICATION NUMBER: 34,616
FILING DATE: THORMATION:
NAME: Charles H. Harris
REILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
RESTERNEY/DOCKET NUMBER: 34,616
REGISTRATION NUMBER: 34,616
RESTERNEY/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FUNCTH: 17 amino acids
                                                                                                                                                                                                                                          ALIGNMENTS
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TYPE: amino acid sequence
STRANDEDNESS: Single
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tes 17; Conservat
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Gaps
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Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 83; DB 2; Length 20; 100.0%; Pred. No. 6.2e-08; Live 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/819,286 FILING DATE: CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/013,599 FILING DATE: 18-MAR-1996 ATTORNEY/AGENT INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                      APPLICATION:
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: TAYLON STAYL
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECHONICATION INFORMATION:
TELECHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids

LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Fish & Richardson P.C.
7: 4225 Executive Square, Suite 1400
La Jolla
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Taylor, Stacy L.
REGIZTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SNKTRIDEANORATKML 17
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Best Local Similarity 100.0
Whiches 17; Conservative
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STATE:
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                                                                                                                                              GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: MARTON: ABSAY for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
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APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: DEPTIDE INHIBITORS OF
CORRESPONDENCE S. 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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100.0%; Score 83; DB 1; L
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMFUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5565699ember 6, 1996
                                                                                                 Sequence 37, Application US/08743894B Patent No. 5965699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
RATORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR ESQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Sequence 4, Application US/08819286

Patent No. 6169074

GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                Length 26;
                                                                                                                                                        0; Indels
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                                                                                                              Query Match
100.0%; Score 83; DB 2; I
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION: 514
PRIOR DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: TAYLOr, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                  1 SNKTRIDEANORATKML 17
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Best Local Similarity 100.
Matches 17; Conservative
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MOLECULE TYPE: peptide
US-08-819-286-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
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USA
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Sequence 10, Application US/08760001 Patent No. 5962637 GENERAL INFORMATION:

RESULT 6 US-08-760-001-10

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington
                                                                                                                                SSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
F: 1100 New York Ave., N.W., Suite 600
Washington
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC. Compatible
COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILNG DATE: Herewith
CLASSIFICATION 1530
PRIOR APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFRERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09015960
Patent No. 6043042
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Paris
Shone, Clifford C.
Hallis, Bassam
James, Benjamin A. F.
Quinn, Conrad P.
NVENTION: TOXIN ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 SNKTRIDEANQRATKML 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
                    APPLICANT: Hallis, Basse
APPLICANT: James, Benjan
APPLICANT: Quinn, Conrad
TITLE OF INVENTION: TOXI
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-371-2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-015-960-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                       STATE: DO
                                                                                                                                                                STREET:
CITY: Wa
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STATE:
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ORGANISM: Artificial sequence
  202-371-2600
              TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                          LENGTH: 70 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-962-360B-11
                                                                                                                                                                               US-09-534-572-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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Sequence 10, Application US/09534572;
Patent No. 6337386;
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
ITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 83; DB 2; Length 70; 100.0%; Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE JOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   1581.0120001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRICE APPLICATION NUMBER: 02/0501279
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.
TELECOMMUNICATION INFORMATION:
TELEPAK: 202-371-2600
TELEPAK: 202-371-2601
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 SNKTRIDEANQRATKML 67
                                                                                                                                                                                                                                                                                                                        70 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Heart Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Neurotoxins
TILE REFERENCE: 003/224/SAP
CURRENT PAPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2010-08-19
PRIOR FILING DATE: 2010-109-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT
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Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 83; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
Query Match
100.0%; Score 83; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 1 7; CTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-09-962-360B-11
                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09962360B Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 SNKTRIDEANQRATKML 112
                                                                                                                                                                  51 SNKTRIDEANQRATKML 67
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STRANDEDNESS: not relevant
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; ORGANISM: Human
US-09-949-016-10671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-949-016-10671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-6311
                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-6311
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Sequence 1, Application US/08819286

Sequence 1, Application US/08819286

GENERAL INFORMATION:

APPLICANT: Montal, Mauricio

TITLE OP INVENTION: PEPTIDE INHIBITORS OF

TITLE OP INVENTION: NEUFOTRANSMITTER SECRETION BY NEURONAL CELLS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: La Jolla

CITY: La Jolla

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
       COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SAFEM: PC-DOS/MS-DOS
SOCTAME: PatentIn Release #1.0, Version #1.25
SUGNARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:
CLASSIFICATION NUMBER: 84.5
ATTORNEY/AGENT INFORMATION:
NAME: SAFELE REPRESENCE/POCKET NUMBER: 8600-0152
REFERENCE/POCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TRNFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TRNFORMATION ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 83; DB 1; I Best Local Similarity 100.0%; Pred. No. 9.1e-07; Matches 17; Conservative 0; Mismatche.
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18 MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: TAYLOY, SLACY L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 07349/0050:
TELEPONE 619/678-5070
TELEPAX: 619/678-5070
TELEPAX: 619/678-509
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TEMBER CHARACTERISTICS:
TEMBER CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 SNKTRIDEANORATKML 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNKTRIDEANORATKWL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 206 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-393-985-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Sequence 10671.

Cursing et al.

RNOWN GENES ASSOCIATED

TITLE OF INVENTION:

PILE REPERENCE: CLOON 1307

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PRIOR PELING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SOFTWARE: PRESEST FOR WINDER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESEST FOR WINDEW: 60/231,498

LENGTH: 219
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100.0%; Score 83; DB 2; Length 206;

Best Local Similarity 100.0%; Pred. No. 9.1e-07;

Matches 17; Conservative 0; Mismatches 0; Indels
                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 SNKTRIDEANQRATKML 203
                                                                                                                                                                                        187 SNKTRIDEANQRATKML 203
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                                                                                                                                                                 1 SNKTRIDEANORATKML 17
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1
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Search completed: April 3, 2006, 15:17:59 Job time : 4.52419 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                         STATE: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08743894B

Sequence 18, Application US/08743894B

Sequence 18, Application US/08743894B

Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: Ages 3 Schmidt

APPLICANT: Ages 4 Schmidt

TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr

NUMBER OF SEQUENCES:
ADDRESSEE: MCMR-JA Atn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CTTY: FORT DETRICK
STRATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER: Apple Macintosh
CONFUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: NO. 5965699ember 6, 1996
CLASSIPICATION NUMBER:
FILING DATE: MICROSOFT WAS APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: MICROSOFT WAS APPLICATION NUMBER:
FILING DATE: MICROSOFT WAS APPLICATION NUMBER:
ATTOMATION NUMBER:
FILING DATE: MICROSOFT WAS APPLICATION NUMBER:
ATTOMATION NUMBER:
MICROSOFT WAS APPLICATION NUMBER:
ATTOMATION NUMBER:
MICROSOFT WAS APPLICATION NUMBER:
MIRCOSOFT W
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Patent No. 565599
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteclytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
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Length 219;
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                                                                         0; Indels
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Query Match
100.0%; Score 83; DB 2;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.4%; Score 80; DB 1; 94.1%; Pred. No. 1.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-714
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 200 SNKTRIDEANQRATKML 216
                                                                                                                                                   1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNKTRIDEANORATKML 17
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TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                    US-08-743-894B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-743-894B-18
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Gaps
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                                                                                                                                                                             OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICTATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION UNDERE: 34,616
REFERENCE/DOCKET MUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 619-2065
TELEFAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNKTRIDEANQKATKML 17
                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 94.1
Matches 16; Conservative
                                                                                               ZIP: 21702-5012
COMPUTER READABLE FORM:
FORT DETRICK
MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                                                                                          21702-5012
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         (without alignments)
57.210 Million cell updates/sec
                                                                                                                                                                     April 3, 2006, 15:49:32 ; Search time 12.7706 Seconds
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1: /SIDSS/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

2: /SIDSS/ptodata/1/pubpaa/USO8 NEW FUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/USO7 NEW FUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/PCT_NEW FUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/USO9 NEW FUB.pep:*

6: /SIDSS/ptodata/1/pubpaa/USO1 NEW FUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/USO1 NEW FUB.pep:*

8: /SIDSS/ptodata/1/pubpaa/USS1 NEW FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180808 seqs, 30441898 residues
                                                                                                                                                                                                                                                                                                                                                      1 XADSNKTRIDEANQRATKMLGSGX 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                          US-09-942-098-90
109
                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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Description	Sequence 36, Appl	Sequence 40, Appl	Sequence 41, Appl	Sequence 36, Appl	Sequence 40, Appl	Sequence 41, Appl	Sequence 11, Appl	Sequence 4, Appli	4	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 225, App	Sequence 20, Appl	50,	12,	32,	Sequence 35, Appl	Sequence 8, Appli	Sequence 34, Appl	34,	, A	37,	Seguence 33, Appl	
ID	US-10-947-071-36	US-10-947-071-40	US-10-947-071-41	US-10-948-097-36	US-10-948-097-40	∹	US-11-195-098-11	US-10-947-071-4	US-10-948-097-4	US-10-947-071-1	US-10-947-071-2	US-10-948-097-1	US-10-948-097-2	US-11-169-041-225	US-10-947-071-20	US-10-948-097-20	US-11-195-098-12	US-10-947-071-35	US-10-948-097-35	US-11-195-098-8	US-10-947-071-34	US-10-948-097-34	US-10-980-346B-6	US-10-980-346B-37	US-10-947-071-33	
DB	9	9	9	9	9	9	7	ø	9	9	9	9	9	7	9	9	7	9	9	7	9	9	9	9	9	
Length	33	33	33	33	33	33	116	203	203	206	206	206	206	206	334	334	116	18	18	24	17	17	17	17	17	
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.5	81.7	81.7	81.7	78.0	78.0	76.1	76.1	76.1	
Score	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	103	83	89	89	85	85	83	83	83	
Result No.	1	8	m	4	ហ	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	

Sequence 33, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 32, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 54, Appl Sequence 60, Appl Sequence 61, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 64, Appl Sequence 66, Appl Sequence 67, Appl Sequence 68, Appl Sequence 61, Appl Sequence 62, Appl Sequence 62, Appl Sequence 63, Appl Sequence 64, Appl Sequence 58, Appl Sequence 58, Appl Sequence 59, Appl Sequence 59, Appl Sequence 50, Appl
6 US-10-948-097-33 6 US-10-980-346B-1 6 US-10-948-097-61 6 US-10-948-097-61 6 US-10-948-097-32 6 US-10-948-097-32 6 US-10-948-097-32 6 US-10-948-097-53 6 US-10-948-097-53 6 US-10-948-097-55 6 US-10-948-097-55 6 US-10-948-097-56 6 US-10-948-097-56 6 US-10-948-097-54 6 US-10-948-097-54 6 US-10-948-097-54 6 US-10-948-097-54 6 US-10-948-097-54 6 US-10-948-097-56 6 US-10-948-097-56 6 US-10-948-097-56
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7.66 7.70 7.70 7.70 7.70 7.70 7.70 7.70
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2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

ALIGNMENTS

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Gaps
   Sequence 36, Application US/10947071
; Sequence 36, Application US20060063221A1
; Publication No. US20060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Steward, Lance
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REPERRENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/10947071
; Sequence 40, Application US/20060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Dudley J.
    APPLICANT: Gilmore, Marcella
    APPLICANT: Steward, Lance
    APPLICANT: Aoki, Kei Roger
    APPLICANT: Aoki, Kei Roger
    TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
    TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
    TITLE OF INVENTION: Lanthanide-Based Substrates
    TITLE OF INVENTION: For Determining Clostridial Toxin Activity
    TITLE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT PILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT CRGANISM: Mus musculus US-10-947-071-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-947-071-40
US-10-947-071-36
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Gaps

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APPLICANT: Verhagen, Marc;
APPLICANT: Werhagen, Marc;
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance;
APPLICANT: Steward, Lance;
APPLICANT: Aoki, Rei Roger;
ITILE OF INVENTION: Pluorescence Polarization Assays For TITLE OF INVENTION: Determining Clostridial Toxin Activity;
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097;
CURRENT PILIG DATE: 2004-09-22;
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Acki, Kei Roger
ITILE OF INVENTION: Flucescence Polarization Assays For
ITILE OF INVENTION: Determining Clostridial Toxin Activity
ITILE OF INVENTION: Determining Clostridial Toxin Activity
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 6; Length 33;
6.8e-12;
les 0; Indels
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Indels
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 109; Local Similarity 100.0%; Pred. No. 6 nes 22; Conservative 0; Mismatches
                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ADSNKTRIDEANORATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ADSNKTRIDEANQRATKWLGSG 33
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                                                                                                                                                                                                                                RESULT 5
US-10-948-097-40
Sequence 40, Application US/10948097
Fublication No. US20060063222A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
                                                                                                              12 ADSNKTRIDEANQRATKWLGSG
                                                                   2 ADSNKTRIDEANQRATKMLGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Carassius auratus
22; Conservative
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US-11-195-098-11
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LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: William, Dudley J.
APPLICANT: William, Dudley J.
APPLICANT: Steward Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lauthanide-Based Substrates and Methods
TITLE OF INVENTION: Lauthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT PILING DATE: 2004-09-21
CURRENT FILING DATE: 2004-09-21
CURRENT PILING DATE: 2004-09-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 33
TYPE: PRT
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                                                                                                                                                                                                                                ; Score 109; DB 6; Length 33;
; Pred. No. 6.8e-12;
0; Mismatches 0; Indels
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Pred. No. 6.8e-12;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40 LENGTH: 33
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; Sequence 41, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
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Sequence 36. Application US/10948097
Publication No. US20060063222A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
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US-10-947-071-41
                                                                                                   ; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40
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CORGANISM: Mus musculus
US-10-948-097-36
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Best Local Similarity
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; Publication No. US20060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Dudley J.
    APPLICANT: Steward, Lance
    APPLICANT: Steward, Lance
    APPLICANT: Acki, Kei Roger
    TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
    TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
    TITLE OF INVENTION: Lanthanide-Based Substrates
    TITLE OF INVENTION: Part Determining Clostridial Toxin Activity
    TITLE OF INVENTION: Por Determining Clostridial Toxin Activity
    TITLE PREFERENCE: 66872-043
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTHARE: FastSEQ for Windows Version 4.0
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                                                                   APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Glimce, Marcella
APPLICANT: Glimce, Marcella
APPLICANT: Glimce, Marcella
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 203
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; Bublication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Abai, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 109; DB 6; Length 2 Best Local Similarity 100.0%; Pred. No. 6e-11; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 109; DB 6; Best Local Similarity 100.0%; Pred. No. 5.9e-11; Matches 22; Conservative 0; Mismatches 0;
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Sequence 4, Application US/10948097
Publication No. US20060063222A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-10-947-071-1
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LENGTH: 206
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US-10-947-071-2
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Sequence 11, Application US/11195098

Publication No. US20050287622A1

GENERAL INFORMATION

APPLICANT: Schmidt, James J.

APPLICANT: Schmidt, James J.

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid

TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid

FILE REFERENCE: 003/224/SaP

CURRENT FILING DATE: 2005-08-02

PRIOR FILING DATE: 2006-09-25

PRIOR PILING DATE: 2000-09-25

PRIOR PILING DATE: 2001-09-25

PRIOR PILING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Apple Macintosh Microsoft Word 6.0

SEQ ID NO 11

LENGTH: 116

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT
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100.0%; Score 109; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Score 109; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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LOCATION: 1
OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
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US-10-948-097-4
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FEATURE: FEATURE: ö

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; ORGANISM: Mus musculus
US-10-948-097-2
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Sequence 1, Application US/10948097

Publication No. US2006006322A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marcella

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

TITLE OF INVENTION: Determining Clostridial Toxin Activity

TITLE OF INVENTION: Determining Clostridial Toxin Activity

TITLE OF INVENTION: 1000 Determining Clostridial Toxin Activity

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 1

LENGTH. 206

LENGTH. 206
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Sequence 2, Application US/10948097

Publication No. US2060063222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marcella

APPLICANT: Steward, Lance

APPLICANT: Steward, Lanc
TITLE OF INVENTION: For Determining Clostridial Toxin Activity FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SSEQ ID NO 2
LENGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-2
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; ORGANISM: Homo sapiens
US-10-948-097-1
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RESULT 14
US-11-169-041-225

JUSTICATION US/11169041

PUDICATION NO. US20060019284A1

PUDICATION NO. US20060019284A1

GENERAL INFORMATION:

APPLICANT: BAISOL-MYCENER SQUIDE COMPANY

TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

PILE REFERENCE: 10001 NP

CURRENT FILING DATE: 2005-06-28

PRIOR APPLICATION NUMBER: 60/584,405

PRIOR PILING DATE: 2004-06-30

NUMBER OF SEQ ID NOS: 527

SEQ ID NO 225

LENGTH: 206

LENGTH: 206
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APPLICANT: Strand, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: APPLICANT: And And Company of the Company o
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Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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              Length 206;
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                                                                                                    0; Indels
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100.0%; Score 109; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0;
         DB 6;
Query Match 100.0%; Score 109; DB 6; Best Local Similarity 100.0%; Pred. No. 6e-11; Matches 22; Conservative 0; Mismatches 0
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, OTHER INFORMATION: Plasmid pobl GFP-SNAP25
US-10-947-071-20
                                                                                                                                                                                                                                                                                      185 ADSNKTRIDEANORATKMLGSG 206
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Publication No. US20060063221A1
GENERAL INPORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-225
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Search completed: April 3, 2006, 15:58:09 Job time: 13.7706 secs

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GenCore version 5.1.7
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Copyright (c) 1993 - 2006 Biocceleration Ltd.	OM protein - protein search, using sw model	April 3, 2006, 15:46:49; Search time 103.266 Seconds (without alignments) 97.107 Million cell updates/sec	118-09-942-098-90
Copyright	rotein search	April 3, 2	11S-09-942-
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1867569 seqs, 417829326 residues 1 XADSNKTRIDEANQRATKMLGSGX 24 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-942-098-90 109 Title: Perfect score: Scoring table: Sequence: Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 12, Appli Sequence 4, Appli Sequence 12, Appli Sequence 109, App Sequence 123, Ap Sequence 123, Ap Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 86, Appli Sequence 88, Appli Sequence 88, Appli Sequence 88, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 12, Appli Sequence 12, Appli	tradic to somewhere
US-09-942-098-12 US-10-261-161-4 US-10-261-161-5 US-10-261-161-5 US-10-318-417-3 US-10-723-860-1223 US-10-723-860-1223 US-10-917-844-2 US-10-917-844-90 US-10-917-844-96 US-10-917-844-86 US-10-917-844-86 US-10-917-844-86 US-10-917-844-86 US-10-917-844-86 US-10-917-844-86 US-09-942-098-88 US-09-942-098-88 US-09-942-098-88 US-09-942-098-88 US-09-942-098-88 US-09-942-098-88 US-09-942-098-88 US-10-917-844-113 US-10-917-844-113	9-/68-60/-01-60
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ALIGNMENTS

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NAME/KEY: MOD_RES
LOCATION: 1
COTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 24
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION
LOCATION: (0)...(0)
LOCATION: (0)...(0)
COTHER INFORMATION: at the C-terminal
US-09-942-024-90
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Best Local Similarity 100.0%; Pred. No. 9.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
Sequence 90, Application US/09942024

publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Apki, Kei Roger

TITLE OF INVENTION: Fert Protease Assays For Botulinum

TITLE OF INVENTION: Fert Protease

TITLE OF INVENTION: Serotype A/E Toxins

FILE REFERENCE: P-AR 4803

CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 90

LENGTH: 24
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; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Fermandez-Salas, Ester
; APPLICANT: APLICANT: Rei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ADSNKTRIDEANORATKMLGSG 23
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US-09-942-024-38
US-09-942-024-38
| Sequence 38, Application US/09942024
| Publication No. US20030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. Sapelicant: APPLICANT: Revard, Lance E. Stering Canding Cand
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 109; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ADSNKTRIDEANQRATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ADSNKTRIDEANQRATKMLGSG 23
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US-09-942-024-38
                                                                                                                                                                                                                                   ; ORGANISM: Carassius auratus US-09-942-024-37
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US-09-942-098-33
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LENGTH: 33
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                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: AD RES
LOCATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 109; DB 3; Length 24; Similarity 100.0%; Pred. No. 9.3e-11; 22; Conservative 0; Mismatches 0; Indels
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Publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Fret Protease Assays For Botulinum

TITLE OF INVENTION: Fret Protease Assays For String

TITLE OF INVENTION: Fret Protease Assays For String

CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 33

LENGTH: 33
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Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
         TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802.
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH: 24
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OTHER INFORMATION: at the C-terminal
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                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-942-024-33
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Best Local Similarity
Matches 22; Conserv
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Length 33;

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US-10-261-161-59

US-10-261-161-59

Sequence 59, Application US/10261161

Publication No. US20040072270A1

SEGNERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: APPLICANT: APPLICANT: Passage For Clostridial Toxins

TITLE OF INVENTION: C11-Based Fluorescence Resonance Energy

TITLE OF INVENTION: C211-Based Fluorescence Resonance Energy

TITLE OF INVENTION: C211-Based Fluorescence Resonance Energy

TITLE OF INVENTION: US-NA 4804

CURRENT APPLICATION NUMBER: US/10/261,161

NUMBER OF SEQ ID NOS: 109

SOFTWARE FastSEQ for Windows Version 4.0

SEQ ID NO 59

LENGTH: 33
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US-JU-261-161

US-JU-261
              TITLE OF INVENTION: Call Based Fluorescence Resonance Energy TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins FILE REFERENCE: PAR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches
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; ORGANISM: Carassius auratus
US-10-261-161-60
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CRGANISM: Carassius auratus
US-10-261-161-59
Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-10-261-161-55
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Best Local Similarity
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100.0%; Score 109; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/09942098
; Sequence 37, Application No. US20030143651A1
; Beblication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Pret Protease Assays
; TITLE OF INVENTION: Pret Protease Assays
; TITLE OF INVENTION: Pret Protease
; TITLE OF INVENTION: PRET PROTEIN
; TITLE PROTEIN TITLE
; TITLE

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Squence 38. Application US/09942098

Publication No. US20030143651A1

GENERAL INFORMATION:

APPLICANT: Steward. Lance E.

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Fernandez-Salas, Ester

TITLE OF INVENTION: Text Roger

TITLE OF INVENTION: Text Protease Assays For Clostridial

TITLE OF INVENTION: Text NOMBER: US/09/942,098

CURRENT APPLICATION UNDER: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOUTHARE: PastSEQ for Windows Version 4.0

SEQ ID NO 38
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Publication No. US20040072270A1
GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
                                                      2 ADSNKTRIDEANQRATKWLGSG 23
                                                                                                                  12 ADSNKTRIDEANQRATKMLGSG 33
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ORGANISM: Carassius auratus

US-09-942-098-37
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US-09-942-098-38
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Best Local Similarity 100.0
Matches 22; Conservative
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Gaps

Length 33;

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JS-10-917-844-38
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| Sequence 37, Application US/2050100973A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. |
| APPLICANT: Adimore, Marcella A. |
| APPLICANT: Adimore, Marcella A. |
| TITLE OF INVENTION: For Botulinum Neurotoxin Protease Assay TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity |
| FILE REFERENCE: 66872-044 |
| CURRENT APPLICATION NUMBER: US/10/917,844 |
| CURRENT FLING DATE: 2004-08-13 |
| PRIOR FILING DATE: 2001-08-28 |
| NUMBER OF SEQ ID NOS: 113 |
| SOFTHARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 37 |
| LENGTH: 23
                                                                                                                                                                                                                                              Sequence 33. Application US/10917844
; Sequence 33. Application US/2050100973A1
; Sequence 33. Application No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.; APPLICANT: Adimore, Marcella A.; APPLICANT: Adimore, Marcella A.; TITLE OF INVENTION: FPP. SANP25 Fluorescence Release Assay
TITLE OF INVENTION: FPP. SANP25 Fluorescence Release Assay;
; TITLE OF INVENTION: FOR DEQUINUM Neurotoxin Protease Activity;
; FILE REPERENCE: 66972-044
; CURRENT FILING DATE: 2004-08-13
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
LEMOTH: 33
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100.0%; Score 109; DB 5; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.4e-10;

Matches 22; Conservative 0; Mismatches 0; Indels
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                    2 ADSNKTRIDEANQRATKMLGSG 23
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Best Local Similarity 100.0%;
Matches 22; Conservative (
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US-10-917-844-37
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US-10-917-844-33
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Sequence 4, Application US/10705857;
Sequence 4, Application US/10705857;
Sequence 4, Application No. US20040147443A1
GENERAL INFORMATION:
TAPLICANT: RENAUT; BEATRIC 5
TITLE OF INVENTION: USE OF A COMBINATION OF COMPONENTS WITH AN INHIBITORY
TITLE OF INVENTION: TREAT WRINKLES AND FINE LINES
TITLE OF INVENTION: TREAT WRINKLES AND FINE LINES
CURRENT APPLICATION NUMBER: US/10/705,857
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: FR 0214183
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: FR 0214183
SOFTWARE: PATENT NOS: 6
SOFTWARE: PATENT NOS: 6
SSOFTWARE: PATENT NO 4
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                                                                      APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Gilmore, Marcella A.
APPLICANT: Gilmore, Marcella A.
TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
FILE REFERENCE: 66872-044
CURRENT APPLICATION NUMBER: US/10/917,844
CURRENT FILING DATE: 2004-08-13
PRIOR PLING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 113
SEQ ID NO 38
LENGTH: 33
LENGTH: 33
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Pred. No. 1.4e-10;
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Sequence 38, Application US/10917844
Publication No. US20050100973A1
GENERAL INFORMATION:
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US-10-917-844-38
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Matches 22; Conservative
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US-08-819-286-8
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Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 11, Appl
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103.582 Million cell updates/sec
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                                                                                       April 3, 2006, 15:31:39 ; Search time 19.156 Seconds
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-962-360B-11

US-09-949-016-6311

US-09-949-016-10671

US-09-949-016-10671

US-09-962-360B-8

US-08-743-894B-1

US-08-743-894B-1
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Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
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1 XADSNKTRIDEANQRATKMLGSGX
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Maximum DB seq length: 2000000000
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Perfect score:
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Patent No. 6169074

GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: DEBROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: TSIA & RIChardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
US-08-743-894B-2
US-08-743-894B-20
US-08-743-894B-24
US-08-743-894B-28
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-34
US-08-743-894B-35
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-45
US-08-743-894B-35
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-38
US-08-743-894B-38
US-08-743-894B-38
US-08-743-894B-38
US-08-743-894B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION
FILING DATE:
CLASSIFICATION: 514
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/013,599
ATTORNEY/AGENT INFORMATION:
NAME: TAYLOR, SECAY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
   70.06
770.06
770.06
770.06
770.06
688.88
688.88
678.99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: La Jo
STATE: CA
COUNTRY: US
ZIP: 92037
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Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-015-960-10
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                                                                                                   Sequence 4, Application US/08819286
Sequence 4, Application US/08819286
Sequence 4, Application US/08819286
Sequence 4, Application
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: NEBPTIDE INHIBITORS OF
TITLE OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.30
SOCTAMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
RAPLICATION NUMBER: US 60/013,599
FILING DATE:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: TAYLON STAY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TO 4:
SEQUENCE: CHARACTERISTICS:
LENGTH: 37 amino acids
THENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shone, Clifford C. APPLICANT: Hallis, Bassam APPLICANT: James, Benjamin A. F. APPLICANT: Quinn, Conrad P. TITLE OF INVENTION: TOXIN ASSAY NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ADSNKTRIDEANQRATKWLGSG 37
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5 ADSNKTRIDEANQRATKMLGSG 26
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; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
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Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TOPOLOGY: linear
) MOLECULE TYPE: peptide
US-08-819-286-4
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                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PILICATION NUMBER: US/09/534,572
FILING DATE: Herewith
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PRIOR APPLICATION DATA:
APPLICATION UNMER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMER: 02-JUN-195
ATTORNEY/AGENT INFORMATION:
NAME: Essend, Robert W.
REGISTRATION NUMBER: 1581.0120003
TELEPHORE: 202-371-2600
TELEPHORE: 202-371-2600
TELEPHORE: 202-371-2601
                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              49 ADSNKTRIDEANORATKMLGSG 70
                                                                                                                                                                                                                                                                                                                                                                                               2 ADSNKTRIDEANQRATKWLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-534-572-10
; Sequence 10, Application US/09534572
Patent No. 6337386
; GENERAL INFORMATION:
                      TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                   Match 100.0%;
Local Similarity 100.0%;
les 22; Conservative 0,
202-371-2600
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                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-015-960-10
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                                                                                                                                                                                      linear
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     TELEPHONE:
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                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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Length 70;

DB 2;

100.0%; Score 109;

Query Match

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APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi TITLE OF INVENTION: Neurotoxins FILE OF INVENTION: NUMBER: US/99/962,360B
CURRENT APPLICATION NUMBER: US 60/235,050
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-09-962-360B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-10; Matches 22; Conservative 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 6.5e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08393985;
Fatent No. 5693476;
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 ADSNKTRIDEANQRATKMLGSG 115
                                                                                                                                                                                                                    US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ADSNKTRIDEANQRATKMLGSG 23
                                                                                                  49 ADSNKTRIDEANQRATKMLGSG 70
                                                                      2 ADSNKTRIDEANORATKWLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94306
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STATE: CA
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ORGANISM: Human
US-09-949-016-10671
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                                                       JS-09-949-016-6311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDEDS: 29
CORRESPONDEDS: 748.6 K SIChardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                              Query Match
100.0%; Score 109; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PC-OMS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CANERNY APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MRA-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRAITON NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEFANE: 619/678-5070
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                 185 ADSNKTRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ADSNKTRIDEANQRATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                   2 ADSNKTRIDEANQRATKMLGSG 23
REGISTRATION NUMBER: 38,615
                                                                                                                i TYPE: amino acids
i TYPE: amino acids
i TOPOLOGY: linear
i MOLECULE TYPE: protein
US-08-393-985-18
                                                                          TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 22; Conserv
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185 ADSNKTRIDEANQRATKMLGSG 206

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Sequence 6311, Application US/09949016

Sequence 6311, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPREMENCE: CLOOD-0.04-14

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 6311

LENGTH: 206
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Sequence 10671, Application US/09949016

BENERAL INFORMATION:

TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRELSEE for Windows Version 4.0

SEQ ID NO 10671

LEMIGTH: 219
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100.0%; Pred. No. 2.5e-10;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.3e-10;
ive 0; Mismatches 0;
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US-09-962-360B-12
; Sequence 12, Application US/09962360B
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Best Local Similarity 100...
Conservative
Conservative
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Best Local Similarity 100.0
Matches 22, Conservative
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APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridis
TITLE OF INVENTION: Hear Throughput Assays for the Proteolytic Activities of Clostridis
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US (09/962,360B)
FRIOR APPLICATION NUMBER: US (0/235,050)
FRIOR APPLICATION NUMBER: US (0/235,050)
FRIOR PILING DATE: 2001-09-25
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 8
LENGTH: 24
TABLE THROUGH THRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fro
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT A
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                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature; LOCATION: 1; COCATION: 1; OTHER INFORMATION: Xaa at 1 is N-fluresceinyl-glycine: 09-09-962-3608-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                       Score 99; DB 2; L
Pred. No. 6.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB 2;
Pred. No. 4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                Query Match
90.8%; Score 99; DB
Best Local Similarity 100.0%; Pred. No. 6.5
Matches 20; Conservative 0; Mismatches
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COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08743894B Patent No. 5965699 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09962360B Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNRTRIDEANQRATRMLGGG 23
                                                                                                                                                                                                                                                                                                                           4 SNKTRIDEANQRATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                                 1 SNKTRIDEANQRATKMLGSG 20
                              not relevant
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85.0%;
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ORGANISM: Artificial sequence
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                           STRANDEDNESS: not re-
TOPOLOGY: linear
MOLECTLE TYPE: peptide
US-08-819-286-9
TYPE: amino acid
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ZIP: 21702-5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-962-360B-8
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                                                                                                  APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOOTHARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 12
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
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APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
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94.5%; Score 103; DB 2;
Best Local Similarity 95.5%; Pred. No. 1.2e-09;
Matches 21; Conservative 0; Mismatches 1
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 ADSNKTRIDEANOAATKWLGSG 115
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; Sequence 9, Application US/08819286
; Patent No. 6169074
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INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
             Patent No. 6762280
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Gaps

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76.1%; Score 83; DB 1; Length 17; 100.0%; Pred. No. 2.7e-07; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                              4 SNKTRIDEANORATKML 20
                                                                                                                                                                                                                                                                                                     1 SNKTRIDEANORATKML 17
                                                                                                                             Query Match 76.1
Best Local Similarity 100.
Matches 17; Conservative
                                          ; FEATURE:
US-08-743-894B-37
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Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Massay for the Proteolytic Activity of Serotype A Neurotoxin fr
ITILE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: MCMR.-JA Atn:John Moran-Patent Atty
STREET: USA MRNC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTR: MARYLAND
COUNTR: PORT DETRICK
STATE: 21702-5012
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Ward 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: Microsoft Word 6.0
CUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFFCATION: 435
FRIOR APPLICATION A15
FRILING DATE:
ATTORNEY/AGENT:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 31,616
REGISTRATION NOMBER: 31,616
REGISTRANDEDNESS: SINGLE
PROPORTION SEG 11,744
REGISTRANDEDNESS: SINGLE
REGISTRANDEDNESS: SINGLE
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NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
LENGTH: amino acids
STRANDEDRESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SNKTRIDEANQRATKML 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
US-08-743-894B-1
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US-08-743-894B-37
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                         2166443 segs, 705528306 residues
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06PC84 BRARE

SN25B CRANU

093579 BRARE

06PC54 BRARE

SN25A CARAU

CY05J6 LATJA

05TZ66 BRARE

09TZ66 BRARE

09TZ66 BRARE

SNP25 MICK

SNP25 MOUSE

SNP25 MOUSE

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Q4S8B5_TETNG
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Maximum Match 100%
Listing first 45 summaries
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QSR690
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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                  Q4rep6 tetracdon n

O8jis7 xenopus lae

009044 mus musculu

070377 rattus norv

Q9d313 mus musculu

Q5r5t6 pongo pygma

Q66d7 brachydanio

Q4v9b6 brachydanio

0010161 homo sapien

0011389 hirudo medi
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99057281; PubMed=9843147;

MEDLINE=99057281; PubMed=9843147;

DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JURI>>3.3.CO;2-Z;

Risinger C., Salaneck B., Soderberg C., Gates M., Postlethwait J.H.,

Risinger C., Salaneck B., Soderberg C., Gates M., Postlethwait J.H.,

"Cloning of two loci for synapse protein Snap25 in zebrafish:

compartison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";

J. Neurosci. Res. 54:563-73(1998).

EMBL; AF091593; AAC64289.1; -; mRNA.

HSSP; Q81384; 1-14A.

SNR; O93578; 49-122.

ENBLSPARGOU000020609; Danio rerio.

ZFIN; ZDB-GRNE-990526-468; snap25a.
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0019717; C:synaptosome; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPero; IPR00197; FIHT Fis.
InterPero; IPR000197; T_SNAPE.
Pfam; PF0035; SNAP-25; 1.
Pfam; PF05739; SNAPE; 1.
Pfam; PF05739; SNARE; 1.
PRINTS; PR01590; HTHFIS.
PROSITE; PS50192; T_SNARE; 1.
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                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Synaptosome-associated protein 25.1 (Fragment).
Name-snap2sa; Synonyma-Snap;
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                            124 AA
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                2015.3 LOGH

08.15.7 XENLA

SNP2.3 MOUSE

SNP2.3 MOUSE

09.03.13 MOUSE

06.01.7 ERANE

06.01.7 ERANE

04.09.6 ERANE

SNP2.3 HURAN

00.01.89 HIRMS
                                                                                                                                                                                               ALIGNMENTS
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22; Conservative (
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2211
2212
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655.1
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664.2
667.6
667.6
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667.6
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77.7
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Gaps

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Length 143; Indels

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NCLECTIDE SEQUENCE.

RC STRAIN=Wild-type; TISSUE-Erye;

RMEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hisher F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rahas S.W., Maruy D.M., Sodergren B.J., Lu X., Glibbs R.A.,

RA Villalon D.K., Maruy D.M., Sodergren B.J., Lu X., Glibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blacksley R.W., Touchman J.W., Gren B.D., Dickson M.C.,

RA Rahesley R.W., Touchman J.W., Gren B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Generation and initial analysis of more than 15,000 full-length human and mouse chan and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                            Pram; PF05733; SNARE; 1.
SMART; SM00397; L.SNARE; 1.
PROSITE; PS50192; T. SNARE; 1.
Hypothetical protein; Synaptosome.
SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                      6043 cm,
100.0%; Score 109; DB 2; L
100.0%; Pred, No. 4e-09;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO; GO: 0019717; C: synaptcsome; IEA.
InterPro; IPR000929; SNAP-25.
InterPro; IPR000727; T SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; L SNARE; 2.
PROSITE; PSS0192; T_SNARE; 2.
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SMR; Q6PC84; 1-77, 123-196.
ZFIN; ZDB-GENE-980526-468; snap25a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ADSNKTRIDEANQRATKMLGSG 143
SMR; Q9GM34; 68-141.
GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PP0035; SNAP-25; 1.
Pfam; PP05739; SNARE; 1.
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Q6PC84;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Blanont C., Skalli Z., Cattolico L., Poulain J.P., Be Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Landet V., Schachter V., Quetier F., Sautin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Hee early vertebrate proto-karyotype."; The early vertebrate proto-karyotype.";
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                               ORFNames=GSTENGO0022427001;
Tetraodon nigroviridis (Green puffer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Actinopterygii, Neopterygii, Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.

Hypothetical protein.

Hypothetical protein.

Hypothetical (Crab eating macaque) (Cynomolgus monkey).

Hypothetical Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Hypothetical Manchontoglires; Primates; Catarrhini;

Cercopithetidae; Cercopithetinae; Macaca.
                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14706, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 109; DB 2; Length 134; 100.0%; Pred. No. 3.7e-09; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049852; BAB16738.1; -; mRNA.
HSSP; Q8T3S4; 1L4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
1; CAAE01014706; CAG03117.1; -; Genomic_DNA.
JENCE 134 AA; 14682 MW; 09109FF243890A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 AA
                                     134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 ADSNKTRIDEANQRATKMLGSG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ADSNKTRIDEANQRATKMLGSG 23
                       O4S8B5_TETNG PRELIMINARY;
Q4S8B5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0
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Q9GM34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GM34 MACFA
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Matches

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PRESENTATION OF THE PROPERTY O

23

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182 ADSNKTRIDEANQRATKMLGSG 203
    2 ADSNKTRIDEANQRATKMLGSG
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
Q6PC54_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration
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                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carassius auratus (Goldfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-i- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PP00835; c.....
Pfam; PP05739; SNARE; 1.
SWART; SN00397; t. SNARE; 2.
PROSITE; PS50192; T. SNARE; 2.

**A CONTROL OF THE CONTROL O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICATY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, a granule cells of the cerebellum.
-!- SIMILARITY: Belongs to the SNAP-25 family.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyg-rich.
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 109; DB 1; Length 203; 100.0%; Pred. No. 5.8e-09; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Risinger C., Larhammar D.; "Multiple loci for synapse protein SNAP-25 in the tetraploid
                                                                        Length 198;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22209 MW; 8FED5099A00E1EC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acad. Sci. U.S.A. 90:10598-10602(1993).
                                                                 ; Score 109; DB 2;
; Pred. No. 5.6e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25B (SNAP-25B)
                                                                                                                                                                                                                                                                                                                203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L22976; AAA16538.1; ; mRNA. PIR; I5481; 150481. HSSP; p13795; 1SFC. SWR; p36978; 7-82, 128-201. InterPro; IPR000928; SNAP-25. InterPro; IPR000727; T_SNARE. Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                  177 ADSNKTRIDEANQRATKMLGSG 198
                                                                                                                                                           2 ADSNKTRIDEANQRATKWLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Retina;
MEDLINE=94068448; PubMed=8248151;
                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carassius auratus (Goldfish)
                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the nerve terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 22; Conserv
Synaptosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=SNAP-B;
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CARBOHYD
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                                                                          Query Match
                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                              SN25B
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"Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Fedingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Synaptosome-associated protein 25.2.
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203 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G) GO:0019717; C:synaptosome; IEA.
InterPro; IPR000228; SNAP-25.
InterPro; IPR000727; T SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SNART; SM00397; t SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
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05-JUL-2004 (TrEMBLrel. 27, Created)
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF001594; AAC64290.1; -; mRNA, HSSP; P60881; 1JTH. SMR; 093579; 7-82, 128-201. ZFIN; ZDB-GENE-980526-392; snap25b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 ADSNKTRIDEANORATKWLGSG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ADSNKTRIDEANQRATKWLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Neurosci. Res. 54:563-573 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.001
                                                                                                                                                                                                                                                                                 Name=snap25b; Synonyms=Snap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEPCS4 BRARE PRELIMINARY;
    O93579 BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
hes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Gaps

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Local Similarity
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=snap-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
COMPBIAS
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                        removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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Q705J6_LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOR DER READ DE LA DE LA DE LA DE LA DE LA DELLA DELLA
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina B., Bonaldo M.F., Caraninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rodan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Amithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ele-FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carassius auratus (Goldfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the nerve terminal. SIMILARITY: Belongs to the SNAP-25 family. SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 109; DB 2; Length 203; ; Pred. No. 5.8e-09; 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059469; AAH59469.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 AA; 22693 MW; 48D7590DD0C1179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-Rel. 29, Last annotation update)
Synaptosomal-associated protein 25A (SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ADSNKTRIDEANQRATKMLGSG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZFIN; ZDB-GENE-980526-392; snap25b. GO; GO:0019717; C:synaptosome; IEA. InterPro; IPR000928; SNAP-25. InterPro; IPR000727; T_SNARE. Pfam; PF00835; SNAP-25; 1. Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMR; Q6PC54; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ADSNKTRIDEANORATKWLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Retina;
MEDLINE=94068448; PubMed=8248151;
                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=Wild-type; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyprinidae, Carassius
NCBI TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=SNAP-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SN25A CARAU
P36977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synaptosome
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Matches
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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A Chen K., Huang X.H.;

R GD, GO.0003700; Firranscription factor activity; IEA.

R GO, GO.0003700; Firranscription of transcription, DNA-dependent; IEA.

R InterPro; IPRO0022; TSNAP-25.

R InterPro; IPRO0022; SNAP-25.

R Pfam; PF05739; SNARE; 1.

R Pfam; PF05739; SNARE; 1.

R SMART; SMO037; TSNARE; 2.

R PROSITE; PSS0192; TSNARE; 2.

R PROSITE; PSS0192; TSNARE; 2.

R SRQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                  EMBL, L22973, AAA16537.1; -; mRNA.

R HSSP; P13795; 1N7S.

R RSP; P6377; 7-202.

R InterPro; IPR000928; SNAP-25.

R InterPro; IPR0037; T_SNAP.

R Pfam; PF0035; SNAP-25; 1.

R Pfam; PF05739; SNARE; 1.

R PROSTITE; PS50122; T_SNARE; 2.

R PROMAIN 138 200 t_SNARE coiled-coil homology 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cys-rich.
458BBECFCFC09189 CRC64;
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Q705JG;
Q705JG;
Q5JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Synaptosomal-associated protein 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 109; DB 2; Similarity 100.0%; Pred. No. 5.8e-09; 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 109; DB 1; 100.0%; Pred. No. 5.8e-09;
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85 92 C
204 AA; 22843 MW;
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us-09-942-098-90.rup

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EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                          Synaptosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
8ynaptosomal-associated protein (SNAP).
Name-snap25a; Synonyms-CTTDARP00000005553; ORFNames=DKEYP-8F4.6-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zeprafish) (Opnio rerio).
Chrinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Name-snap25a; Synonyms=OTTDARP00000005690; ORFNames=DKEYP-8F4.6-002;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio retio (Zebrafish) (Danio rerio).
Brachydanio Retazoa; Mopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; Bx465184; CAH69032.1; -; Genomic_DNA.
EMBL; Bx470246; CAI21360.1; -; Genomic_DNA.
EMBL; Bx470246; CAI21360.1; JOINED; Genomic_DNA.
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
[2]
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX465184; CAH69031.1; -; Genomic_DNA.
EMBL; BX470246; CAI21359.1; -; Genomic_DNA.
EMBL; BX470246; CAI21359.1; JOINED; Genomic_DNA.
EMBL; BX45184; CAH69031.1; JOINED; Genomic_DNA.
EMBL; BX465184; CAI21399.1; JOINED; Genomic_DNA.
EMBL; BX465184; CAI2139.20.2
EMBL; BX465184; CAI2139.20.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 100.0%; Score 109; DB 2; Local Similarity 100.0%; Pred. No. 5.8e-09; tes 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA.
                                                                           204 AA
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                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR00077; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
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PROSITE; PS50192; T_SNARE; 2.
                                                                     QSTZ66_BRARE PRELIMINARY;
QSTZ66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSTZ65_BRARE PRELIMINARY;
QSTZ65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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1D 05TZ65 BR
DT 01-FBB-2C
DT 01
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Matches
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Event=Alternative splicing; Named isoforms=2; Comment=1soforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP25 CHICK STANDARD; PRT; 206 AA.
P60878; P13795; P36974; P70558; Q8IXK3; Q96FM2; Q9BR45;
P60878; P13795; P36974; P70558; Q8IXK3; Q96FM2; Q9BR45;
P601-JAN-1990 (Rel. 13, Created)
10-FB-1991 (Rel. 17, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
35 kba protein) (Super protein) (SUP).
Name-SNAP25; Synonyme-SNAP;
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of the chicken gene for SNAP-25 reveals duplicated exon encoding distinct isoforms of the protein.";
J. Mol. Biol. 233:67-76(1993).
-!- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=White leghorn; TISSUE=Retina;
MEDLINE=91126080; PubMed=1992470;
Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson M.C.; "Expression of a conserved cell-type-specific protein in nerve terminals coincides with synaptogenesis."; proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indele
                                                                                                                                                                                                                                                                                                                                                    204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
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MEDLINE-93389738; PubMed=8377193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 109; DB 2; 100.0%; Pred. No. 5.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
SMR; QSTZ65; 7-83, 129-202.
Ensembl; ENSDARG0000000609; Danio rerio.
ZFIN; ZDB-GENE-980526-468; snap25a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
                                                                                              GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP.25.
InterPro; IPR000727; T SNARE.
Pfam; PP00835; SNAP-25; 1.
SNART; SN00397; t SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 ADSNKTRIDEANQRATKMLGSG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ADSNKTRIDEANQRATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=SNAP-25a;
IsoId=P60878-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P60878-1, P13795-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B)
                                                                                                 rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roders
  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                       Cys-rich.
Cleavage (by BONT/E) (By similarity).
Cleavage (by BONT/E) (By similarity).
Phosphoserine (By similarity).
ERIEEGMDQINKDMKEAEKNLTDLGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP25 HUMAN STANDARD; PRT; 206 AA.
P60880; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 13, Created)
01-FB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated brotein) (SUP).
Name-SNAP25; Synonyms-SNAP;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMNHINQDMKEAEKNLKDLGKCCGLFI (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 109; DB 1; Length 206; 100.0%; Pred. No. 5.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                   t-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                           InterPro; IPR000328; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00335; SNAP-25; 1.
SMART; PF05739; SNARE; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                         L; 109251; AAA49070.1; JOINED; Genomic_DNA.
L; 109256; AAA49070.1; JOINED; Genomic_DNA.
L; 109253; AAA49070.1; JOINED; Genomic_DNA.
L; 109254; AAA49071.1; -; Genomic_DNA.
L; 109254; AAA49071.1; JOINED; Genomic_DNA.
L; 109259; AAA49071.1; JOINED; Genomic_DNA.
L; 109252; AAA49071.1; JOINED; Genomic_DNA.
L; 109252; AAA49071.1; JOINED; Genomic_DNA.
L; 109258; AAA49071.1; JOINED; Genomic_DNA.
L; 109250; AAA49071.1; JOINED; Genomic_DNA.
L; 109250; AAA49071.1; JOINED; Genomic_DNA.
L; 109250; AAA49071.1; JOINED; Genomic_DNA.
                                                                                                                                          AAA49070.1; JOINED; Genomic DNA
AAA49070.1; JOINED; Genomic DNA
AAA49070.1; JOINED; Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                       EMBL; M57957; AAA49072.1; -; MRNA.
EMBL; L09253; AAA49070.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNAP-25a)
                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Repeat; Synaptosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 ADSNKTRIDEANQRATKWLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ADSNKTRIDEANQRATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 AA; 23315 MW;
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SMR; P60878; 7-83, 131-204.
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202
92
181
138
187
89
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MOD_RES
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Altaunner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bromstein M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan R.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Skeletal muscle;
MEDLINE-96332494; PubMed-8760387;
Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
Ward C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94333829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2; Zhao N., Hashida H., Takahashi N., Sakaki Y.; "Cloning and sequence analysis of the human SNAP25 cDNA."; Gene 145:313-314(1994).
MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
                                                               Bark I.C., Wilson M.C.; "Human CDNA clones encoding two different isoforms of the nerve "Human CDNA clones may reterminal protein SNAP-25."; Gene 139:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 317:945-954(1996).
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RESULT a ઠે This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not Event=Alternative splicing, Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39; Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human X.-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX WITH STX1A; CPLX1 AND VAMP2, AND NWR ANALYSIS.
MEDLINE=21822661; Pubmed=11832227; DOI=10.1016/S0896-6273(02)00583-4; Chen X., Tomchick D.K., Kovrigin E., Arac D., Machius M., Suedhof T.C., Rizo J.;
"Three-dimensional structure of the complexin/SNARE complex."; neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion. SUBUNIT: Part of the SNARE core complex containing SNAP25. VAMP2 and STAIA. This complex binds CPLAI. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity). GO: 000726; P:neurotransmitter secretion, NAS.
GO: 000726; P:neurotransmitter uptake; NAS.
GO: GO:00050796; P:nequlation of insulin secretion; TAS.
GO: GO:0007268; P:synaptic transmission; NAS.
GO: GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE. and Sequence-VSP 006186;
-1-TISSUB SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, portine nuclei, argranule cells of the cerebellum.
-1-FTM: Palmicoylated (By similarity).
-1-SIMILARITY: Belongs to the SNAP-25 family.
-1-SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains. Neuron 33:397-409(2002). -!- FUNCTION: t-SNARE involved in the molecular regulation of QBIUM5:HIP14; NDEXP=1; IntAct=EBI-524785, EBI-524753; ALTERNATIVE PRODUCTS: and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) EMBL; AL023913; CAC34534.1; -; Genomic_DNA. EMBL; AL023913; CAC34535.1; -; Genomic_DNA. EMBL; AL023913; CAD56158.1; -; Genomic_DNA. EMBL; AL023913; CAB42866.1; -; Genomic_DNA. EMBL; BC010647; AAH10647.1; -; mRNA. EMBL; L19760; AAC37545.1; -; mRNA. EMBL; L19761; AAC37546.1; -; mRNA. EMBL; D21267; BAA22370.1; -; mRNA. Name=SNAP-25a; IsoId=P60880-2, P13795-2; IsoId=P60880-1, P13795-1; Sequence=Displayed; H-InvDB; HIX0015639; -. PIR; I53735; I53735. PIR; I67823; I67823. INTERACTION:

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                                                                                                                                                                                                                                                 Phosphothreonine (By similarity).
Phosphoserine (By similarity).
ERIEEGMDQINKDMKEAEKNITDIGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP25 MACMU STANDARD; PRT; 206 AA.
P60877; P13795; P36974; P70558; Q8IXK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 13, Created)
01-FRB-1991 (Rel. 17, Last sequence update)
13-SRB-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMNHINODMKEAEKNLKDLGKCCGLFI (in 180form SNAP-25a).
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Jensen M.J., Smith L.A.;
Jensen M.J., Smith L.A.;
Jensen M.J., Smith L.A.;
Jensen M.J., Smith L.A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Pfam; PF00835; Sim.
Pfam; PF05739; SNARE; 1.
SMART; SM0397; t SNARE; 2.
PROSITE; PS50192; T SNARE; 2.
3D-structure; Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat; Synaptosome.
Palmitate; Phosphorylation; L-SNARE coiled-coil homology 1.
19 2. 1-SNARE coiled-coil homology 2.
T-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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142 201
202 202
206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 109; DB 1; 100.0%; Pred. No. 5.8e-09;
                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_006186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF240770; AAF64477.1; -; mENA.
SMR; P60877; 7-83, 131-204.
Interpro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 ADSNKTRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ADSNKTRIDEANQRATKMLGSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9544;
                                                                                                                                                                                 140
85
180
138
187
58
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                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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HELIX
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STRAIN-C57BL/6J; TISSUE-Medulla oblongata;

X MEDLINE-22354683; PUDMC41246681; DOI-1013 (nature01266;

A MEDLINE-22354688; PUDMC41246681; DOI-1013 (nature01266;

A MIKAdO I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikado I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,

A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Fletcher C.F., Porrest K.S.,

A Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Eletcher C.F., Porrest K.S.,

Grassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagasa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescole G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP25 MOUSE STANDARD; PRT; 206 AA.
P60879; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
P01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 kDa protein) (Super protein) (SUP).
Name=Snap25; Synonyms=Snap;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
Bloom F.E., Wilson M.C.,
"The identification of a novel synaptosomal-associated protein, SNAP-
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                     Cleavage (by BONT/E) (By similarity). Phosphothreonine (By similarity). Phosphoserine (By similarity). FBED28082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ILS, and ISS;

MEDLINE-2156310. PubMed=11471062; DOI=10.1007/s00335-001-1001-x;

Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J., Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;

"High-throughput sequence identification of gene coding variants within alcohol-related QTLs.";

Mamm. Genome 12:657-663(2001).
                                                                                                                                                                                                                                                                                                                                                                   ö
                                        SMART, SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Colled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
                                                                                                                               t-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
Cys-rich.
                                                                                                                                                                                                                                                                                                                ; Score 109; DB 1; Length 206; ; Pred. No. 5.8e-09; 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25, differentially expressed by neuronal subpopulations.";
J. Cell Biol. 109:3039-3052(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 ADSNKTRIDEANQRATKWLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                2 ADSNKTRIDEANORATKMLGSG 23
                                                                                                                                   81 t-
202 t-
92 CY
181 CI
181 Ph
187 Ph
23315 MW;
                                                                                                                                                                                                                                                                                                                    100.0%;
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                 22, Conservative
                                                                                                                                                         140 2
85
180 1
138 1
187 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                   Synaptosome.
                                                                                                                                                                                                                           MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                   COMPBIAS
                                                                                                                                        DOMAIN
                                                                                                                                                                DOMAIN
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RP NUCLECATIDE SEQUENCE [LARGE SCALE MENA] (ISOFORM SNAP-25A).

RC STRAIN=C57BL/6; TISSUE=Eye;

RTAIN=C57BL/6; TISSUE=Eye;

RA MININ=2338827; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Alteshul S.F., Zeoberg B., Bonaldo M.F., Rasvant T.L., Scheetz T.E.,

RA Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,

RA Bosak S.A., McSwan B.J., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.A., McSwan P.J., McKernan K.J., Malk V.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley R.C., Shevchenko Y., Boutfard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Werardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Weils C.,
Milming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Myana Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Saro K.,
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Myasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Birney E., Hayaahizaki Y.,
Hany E., Hayaahizaki Y.,
"Analysis of the mouse transcriptome based on functional annotation of
I. Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion. Subsurir: Part of the STARE core complex containing SNAP25, vAMP2 and STXIA. This complex binds CPLXI. Interacts with TRIM9, RIM81, STXIA and VAMP8 (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and protein kinase A.";
FEBS Lett. 532:52-56(2002).
-!- FUNCTION: t-SNARE involved in the molecular regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pubmed=10195194; DOI=10.1038/5673;
Llardi J.M., Mochida S., Sheng Z.-H.;
Snapin: a SNARE-associated protein implicated in synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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IsoId=P60879-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P60879-1, P13795-1;
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us-09-942-098-90.rup

Search completed: April 3, 2006, 15:46:23 Job time : 125.743 secs

185 ADSNKTRIDEANQRATKWLGSG 206

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 3, 2006, 15:30:10 ; Search time 12.9908 Seconds (without alignments) 177.756 Million cell updates/sec Run on:

Title: Perfect score:

US-09-942-098-90 109 1 XADSNKTRIDEANQRATKMLGSGX 24 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description			synapse protein SN	synaptosomal-assoc	nerve terminal pro	nerve terminal pro	synaptosomal-assoc	synapse protein -	SNARE protein 23 -	synaptosomal-assoc	vesicle-membrane f	vesicle-membrane f	conserved hypothet	hypothetical prote	adhesin homolog lm		DNA-directed RNA p	hypothetical prote	lipoprotein [impor	peptidoglycan boun	comE operon protei	w	hypothetical prote	probable tape-meas	hypothetical prote	molybdopterin bios	outer membrane lip	hypothetical prote	ப	dihydropteroate sy
	QI		I50481	I50480	A37861	153735	167823	A33623	I50552	JC5512	A49708	JC5297	JC5296	D87525	T26553	AC1153	T51833	A29959	T29999	G90551	AD1512	AH3356	E81436	576238	AG1360	C83655	A81299	A33854	AB1996	84	E72425
	DB	1	7	~	~	7	N	~	~	~	~	~	~	~	~	~	7	7	7	~	N	7	~	~	~	~	~	~	7	7	0
	Length		203	204	206	206	206	206	210	210	29	158	211	296	234	1582	335	1361	2288	642	1578	278	401	1578	1787	109	148	83	219	258	278
æ	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	64.2	57.8	55.5	54.1	54.1	45.0	44.0	43.1	42.2	42.2	42.2	41.3	41.3	40.4	40.4	40.4	40.4	39.4	39.0	38.5	38.5	38.5	38.5
	Score		109	109	109	109	109	109	70	63	60.5	29	59	49	48	47	46	46	46	45	45	44	44	44	44	43	42.5	42	42	42	42
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Gaps

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Query Match
100.0%; Score 109; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C

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hypothetical prote angiotensin precur	near snock / Un pro outer membrane pro	hypothetical prote ADP-ribosylation f	ADP-ribosylation f	hypothetical profe	major capsid proce	hypothetical prote	replication protei	repB protein (U809	hypothetical prote	probable outer mem	ezy-1 protein prec	pre-mRNA splicing
S50562 JC2318	T34037 H70347	T33167 A45422	JC4946	T09047	T13220	T16532	AE3039	G98246	T32127	B71963	B48210	S64386
999	20	9 7	11 2	11 2	11 2	36 2	17 2	17 2	3 2	18 2	3 2	2 2
420	9 9	105	18	2	56	26	33	33	35	4.3	45	4
38.5 38.5	38.5	38.5	38.1	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6
22	22					41	41	41	41	41	41	41
4. 4.	4. 4.	41,4	41.5	•	•	•	•	•	•	•	•	•
30 31	33 33 33	6. E.	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Best Loc Matches

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synapse protein - marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50552
R;Risinger, C.; Blomqvier, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.; J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Bvolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shc A;Reference number: A49513; MUD:94043281; PMID:8226991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; P. J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differer A;Reference number: A33623; MUID:90078337; PMID:2592413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UP10000135AFE; GB:L22020; NID:g431296; PIDN:
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JC5512
SNARE protein 23 - mouse
SNARE protein 23 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Okaz Biochem. Biophys. Res. Commun. 214, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Muncl8c.
A;Reference number: JC5512; MUID: 97312558; PMID: 9168999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:920(
                                                                                                                                                                                                                                                                                                                                                                                                                  synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
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                                                                                         Length 206;
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                                                                                                                                                Indels
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                                                                                                                                                ö
                                                                                      Score 109; DB 2;
Pred. No. 6.2e-10;
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Pred. No. 0.0012;
1; Mismatches 3
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                                                                100.0%; 5000.
100.0%; Pred. No. 0.
0; Mismatches
A,Cross-references: GDB:355671; OMIM:600322
A,Map position: 20p11.2-20p11.2
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193 DMNKARIDEANKHATKML 210
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Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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A; Status: preliminary
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C;Species: Homo Bapiens (man)
C;Date: 29-May-1998 #Bequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 167823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: IS3735; MUID:94156217; PMID:8112622
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R;Bark, I.C.; Wilson, M.C.
Espene 139, 291-292, 1994
A;Titels: Human cDNA clones encoding two different isoforms of the nerve terminal protein A;Reference number: IS3735; WUID:94156217; PMID:8112622
                                                                                                                                                                                                                                   RiCatsicas, S.; Larhammar, D.; Blomgvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C. Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid A;Reference number: A37861; MUID:91126080; PMID:1992470
                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Rebidues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UP10000001103; GB:M57957; NID:g212673; PIDN:
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A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UP1000002B3DD; GB:L19760; NID:g307425; PIDN
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                                                                                                                    synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nerve terminal protein - human
C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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Pred. No. 6.2e-10;
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A;Molecule type: mRNA
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A;Map position: 20p11.2-20p11.2
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Best Local Similarity 100.C
Matches 22, Conservative
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C;Genetics:
A;Gene: GDB:SNAP
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conserved hypothetical protein CC2229 [imported] - Caulobacter crescentus conserved hypothetical protein CC2229 [imported] - Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C; Accession: D87525 R; Miscernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolone B.; Laub, M.T.; Dedson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proco. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A; Title: Complete Genome Sequence of Caulobacter crescentus. Apreference number: A87249; MuID:21173698; PMID:11259647
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C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26553
A;Gardner, A.
Submitted to the EMBL Data Library, January 1998
A;Gardner, A.
A;Accession: T26553
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T26553
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 1-234 <WIL>
A;Residues: 1-234 <WIL>
A;Residues: 1-234 <WIL>
A;Residues: 1-234 cone Y22F5A
A;Experimental source: clone Y22F5A
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 ir A;Reference number: JC5296; MUID:9724437; PMID:9070898
A;Accession: JC5296
A;Accession: JC5296
A;Actus: nucleic acid sequence not shown; translation not shown
A;Acleule type: mRNA
A;Residues: 1-211 <MOL>
A;Residues: 1-211 <MOL>
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cent
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54.1%; Score 59; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. No. 0.068;
Matches 12; Conservative 4; Mismatches 5; Indels
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45.0%; Score 49; DB 2;
Best Local Similarity 55.6%; Pred. No. 4;
Matches 10; Conservative 2; Mismatches
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42.1%; Pred. No. 4.4;
tive 6; Mismatches
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247 KRNVDWANQLKTKLAGSG 264
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A;Introns: 51/3; 82/1; 165/2; 213/3
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Best Local Similarity 42...
Best Local 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-296 <STO>
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A, Gene: CESP: Y22F5A.3
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C; Comment: This protein is involved in regulating exocytosis in human neutrophils, a cert C; Comment: This protein is involved in regulating exocytosis in human neutrophils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C)Accession: A49708

R;Birz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; J. Blool. Chem. 269, 1617-1620, 1994

A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.

A;Reference number: A49708; MUID:94124495; PMID:8294407
                          A,Molecule type: mRNA
A,Residues: 1-210 cARA>
A,Cross-references: UNIPROT:009044; UNIPARC;UPI0000022B5C; DDBJ:AB000822; NID:g2189950;
C,Comment: This protein is involved in the insulin-induced translocation of vesicles con
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A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5297
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C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5296
R;Mollinedo, F; Lazo, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synaptosomal-associated 25K protein - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Homo sapiens (man)
C.Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C.Accession: JC5297
R.Mollinedo, F., Lazo, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.5%; Score 60.5; DB 2; Length 29; 68.2%; Pred. No. 0.0046; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                            Length 210;
                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                         57.8%; Score 63; DB 2;
61.9%; Pred. No. 0.015;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vesicle-membrane fusion protein SNAP-23A - human C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vesicle-membrane fusion protein SNAP-23B - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-29 <BIN>
A;Cross-references: UNIPARC:UP1000017C9D4
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ADTNRDRIDIANARAKKLIDS 158
                                                                                                                                                                                                                                                                                                                                                  190 ADTNKNRIDIANTRAKKLIDS 210
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Best Local Similarity 57.19
Matches 12; Conservative
                                                                                                                                                                                                            Best Local Similarity 61.94
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 68.2
nes 15; Conservative
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adhesin homolog lmo0627 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1153
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1153
A;Residues: 1-1582 cGLA>
A;Genetics: A;Genetics: Strain EGD-e
C;Genetics: A;Genetics: A;Geneti
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
B; Liu, Q; Kasuga, M.; Sakuma, Y.; Abe, H.; Miura, S.; Yamaguchi-Shinozaki, K.; Shinozak Plant Cell 10, 1391-1406, 1998
Plant Cell 10, 1391-1406, 1998
A; Fill 10, 1391-1406, 1998
A; Reference number: 225477
A, Accession: T51833
A; Accession: T51833
A; Residues: 1-335 <LIU>A; Residues: 1-345 <LIUA>A; Res
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Description: specifically bound to the DRE sequence in vitro and activated t he transd
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A;Experimental source: strain Colombia
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43.1%; Score 47; DB 2; Length 1582;
Best Local Similarity 45.5%; Pred. No. 50;
Matches 10; Conservative 3; Mismatches 9; Indels
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Job time : 15.9908 secs
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214 AQSNEVRESANKRAKNLI 232
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April 3, 2006, 15:27:08 ; Search time 123.083 Seconds (without alignments) 85.675 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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109
1 XADSNKTRIDEANQRATKWLGSGX
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geneseqp2003bs:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aae36735 Fret subs	Abw01791 FRET subs	Aaw30099 Neurotran	_	_	-	Goldfi	_	_	~	<u>-</u>	σ	Aeal4927 Goldfish		Aea14928 Goldfish	_	-	Aab15584 Human SNA	Adp13169 SNAP 25 p	_	Aao15165 Clostridi	_	Τ.	Adm97001 Goldfish
SUMMARIES	ΩI	AAE36735	ABW01791	AAW30099	AAE36682	AAE36683	AAE36678	ABW01739	ABW01734	ABW01738	ADM97054	ADM97053	ADM97049	AEA14927	AEA14923	AEA14928	AAW30097	AAR86823	AAB15584	ADP13169	AEA15002	AA015165	ADN11044	ABW01715	ADM97001
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	& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109
	Result No.	-	10	m	4	S	4	7	· co	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

•	_	Aae36662 Human SNA Aae36667 Rat VAMP- Ade54280 Rat Prote	Rat Huma Rat	Ades4274 Rat Prote Ades4286 Human Pro Ades4284 Rat Prote Ades4272 Rat Prote	
AEA14904 AAW30103 AAW43426	AAW79198 AAU00246 AAU00253 AAU00252	AAE36667 AAE36667 ADE54280	ADE54288 ADE54276 ADE54290 ADE54282	ADE54274 ADE54286 ADE54284 ADE54272	ABW01703 ABW01703 ABW01708
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25 26 27	30 30 31	333	35 34 38	0 4 4 4 0 0 1 0	4 4 4 4 2 6 4 8

ALIGNMENTS

/note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 90 in the sequence listing of the specification" Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site. Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 90 it he sequence listing of the specification" Fret substrate peptide #6 used in the invention. Aoki KR; Example 1; Page 115; 168pp; English. Location/Qualifiers Ź Steward LE, Fernandez-Salas E, AAE36735 standard; peptide; 24 28-AUG-2001; 2001US-00942024. 22-AUG-2002; 2002WO-US027145. (first entry) (ALLR) ALLERGAN INC. WPI; 2003-290198/28. WO2003020948-A2 Key Modified-site Modified-site Unidentified 07-AUG-2003 13-MAR-2003. cosmetic. AAE36735; RESULT 1

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BONT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance appetrum overlapping the emission spectrum of the donor fluorophore and abont A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the procease activity of any clostridial toxin including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast samples of the invention of processed foods, beverages, animal feed, soil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRET substrate #4 to analyse proteolytic activity of botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 109; DB 6; Length 24; 100.0%; Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local Similarity 100.0
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amide"
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Modified-site
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ABM
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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.

Aoki KR;

Steward LE, Fernandez-Salas E,

WPI; 2003-829791/77.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    suppressonal associated protein (SNRP-25), and is a inhibitory agent of the invention. The agents of the invention inhibit secretion of the invention. The agents of the invention inhibit secretion of unconcensuiter from neuronal cells and is an excitation-secretory uncoupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally any (I) that inhibits 50% of catecholamine secretion from bovine chromaffin cells at a concentration of 10 microM, especially 0.25 microM, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit release of neurotransmitters from synaptic vesicles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering substance P to brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or immunogenic and are more readily
                                                           assaying for the protesse activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteclytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
                                                   The present invention provides clostridial toxin substrates useful in
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Excitation-secretory uncoupling peptide(s) for inhibiting nuscle neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence corresponds to residues 181-206 of the human 25 kD
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                                                                                                                                                                                                                        Length 24;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                    100.0%; Score 109; DB 7;
100.0%; Pred. No. 1.9e-10;
live 0; Mismatches 0;
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               Example 1; Page 29; Opp; English
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                                                                                                                                                                                                                                                              22; Conservative
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                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                       Sequence 24 AA;
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AAW30099
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; Score 109; DB 2; ; Pred. No. 2.1e-10; 0; Mismatches 0;

Length 26; Indels

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available. Their therapeutic effect lasts for several days or weeks,
lower doses or less frequent treatments are required
                                                       2 ADSNKTRIDEANQRATKMLGSG 23
                                                                ADSNKTRIDEANQRATKMLGSG 26
                                                                                                   AAE36682 standard; peptide; 33 AA
                               100.001
                                                                                                                                                                                                                                                                             28-AUG-2001; 2001US-00942024
                                      100.08;
                                                                                                                           (first entry)
                                                                                                                                       Goldfish SNAP-25A peptide
                                            Conservative
                                                                                                                                                                                                                                                                                          (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                  WPI; 2003-290198/28.
                                     Local Similarity
hes 22; Conserv
                                                                                                                                                                            Carassius auratus
                                                                                                                                                               rent; cosmetic.
                                                                                                                                                                                                                                        WO2003020948-A2
                    Sequence 26 AA;
                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                       Cleavage-site
                                                                                                                          07-AUG-2003
                                                                                                                                                                                                                                                                                                      Steward LE,
                                                                                                               AAE36682;
                                Query Match
                                            Matches
                                                                                           AAE36682
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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BoNT/A/B) substrates which comprises a donor fluorophore, an acceptor having an absorbance pectrum overlapping the emission spectrum of the donor fluorophore and a pectrum of clasavage site intervenes between the donor fluorophore and acceptor the clasavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurocoxins include VAMP (synaptobrevin), SMAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeWT) in a sample including bacterial, baculoviral and yeast typate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site. Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; 7. .8 /note= "BoNT/E sensitive cleavage site" 24. .25 /note= "BoNT/A sensitive cleavage site" 25. .26 /note= "BoNT/C sensitive cleavage site" Ř Aoki Disclosure; Page 42; 168pp; English. Location/Qualifiers Fernandez-Salas E, 22-AUG-2002; 2002WO-US027145.

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e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is goldfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldfish; clostridium toxin; protease activity; botulinum toxin; BONT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                     Length 33;
                                                                                                                                                                                                                                                                         Indels
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'note= "BoNT/E sensitive cleavage site"
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                                                                                                                                                                                                                       Score 109; DB 6;
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                              SNAP-25A peptide used in the invention
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                                                                                                                                                                                                                                                                                                                                                          12 ADSNKTRIDEANQRATKMLGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE36683 standard; peptide; 33
                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                            Query Match
Best Local Similarity
Local Similarity
Set Local Similarity
Tocal Similarity
Tocal Similarity
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25. .26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reNT; cosmetic.
                                                                                                                                                                      Sequence 33 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BONT/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BONT/B recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is
lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is goldfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, clostridium toxin, protease activity, botulinum toxin, BoNT; TeNT,
tetanus toxin, VAMP; synaptobrevin, SNAP-25, syntaxin, pharmaceutical;
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                        Length 33;
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/note= "BoNT/E sensitive cleavage site"
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/note= "BONT/C sensitive cleavage site"
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                                                                                                                                                                                        100.0%; Score 109; DB 6; 100.0%; Pred. No. 2.8e-10;
                                                                                                                                                                                                                       Mismatches
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                                                                                                                      SNAP-25B peptide used in the invention
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                                                                                                                                                                                                                                                                            ADSNKTRIDEANQRATKMLGSG 33
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cosmetic; mouse; rat.
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exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the processe activity of any clostridial toxin including botulinum toxins of all serotypes and tetamus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is SNAP-25 peptide used in the invention
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Les 22; Conservative
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(FERN/) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
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Best Local Similarity
Matches 22; Conserv
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ABW01734 RESULT

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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
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100.0%; Pred. No. 2.8e-10;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                       (STEW/) STEWARD L E.
(FERN/) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
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Carassius auratus.
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22; Conservative 0
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(FERN) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steward LE,
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Matches

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RESULT 9

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Gaps

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Length 33; Indels

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04-SEP-2003; 2003WO-US028092.
                                                                                                                                                         WPI; 2004-340456/31.
                                                                                                                                                    Fernandez-Salas E,
                                                                                                                            WO2004029576-A2
                                                                Sequence 33 AA;
                                                                                                                                 08-APR-2004
                                                                                                    ADM97053;
                                                                                          RESULT 11
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The invention relates to a method of determining (MI) clostridial toxin activity, comprising contacting cell with sample comprising clostridial activity, comprising contacting cell with sample comprising clostridial coxin measurements. (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening clostridial toxin recognition sequence with cleavage site intervening transfer is exhibited between fluorophore and acceptor, exciting the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell is indicative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the contact cell is indicative of clostridial toxin activity. (MI) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (MI) is an automated high-throughput assay. (MI) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and protease activity. In the method MI, the clostridial toxin substrate is a botulinum toxin substrate comprising a BONT/A, BONT/B, BONT/E, BONT/F, BONT/C, BONT/F, Corresponds to a recognition sequence for a botulinum toxin used as the clostridial Disclosure; SEQ ID NO 60; 188pp; English coxin substrate

ö 100.0%; Score 109; DB 8; Length 33; 100.0%; Pred. No. 2.8e-10; ive 0; Mismatches 0; Indels 2 ADSNKTRIDEANQRATKMLGSG 23 12 ADSNKTRIDEANORATKWLGSG 33 Query Match Best Local Similarity 100.0 Matches 22; Conservative

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Gaps

Botulinum toxin substrate recognition sequence #38. ADM97053 standard; peptide; 33 AA. 01-JUL-2004 (first entry)

clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food

Carassius auratus.

27-SEP-2002; 2002US-00261161

(ALLR) ALLERGAN INC

Aoki

Steward LE,

Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance transfer of contacted cell. energy

Disclosure; SEQ ID NO 59; 188pp; English.

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donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (MI) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (MI) is an automated high-throughput assay. (MI) reduces the need for animal toxicity studies and serves to analyze contitiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and protease activity. In the method MI, the clostridial toxin subserate is a botulinum toxin substrate selected from a BOMT/A, BOMT/B, BOMT/C, BOMT/F, BOMT/F, BOMT/G or TeMT substrate comprising a BOMT/A, BOMT/B, BOMT/C, BOMT/B, BOMT/C, BOMT/C
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                                        comprising clostridial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food
The invention relates to a method of determining (MI) clostridial toxi activity, comprising contacting cell with sample comprising clostridia toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM97049 standard; peptide; 33 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ADSNKTRIDEANQRATKMLGSG
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-340456/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus.
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absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in contacted cell relative to a control cell, where a difference in contacted cell is indicative of the contacted cell as compared to the contact cell lysate, isolated clostridial toxin activity. Where the sample is a crude cell tysate, isolated clostridial toxin, formulated clostridial toxin crudices the need for animal toxicity studies and serves to analyze reduces the need for animal toxicity studies and serves to analyze controling functions such as binding a cellular uptake of the toxin, the clostridial toxin substrate is a botulinum toxin substrate of the toxin, selected from a BowT/A, BowT/B, BowT/F, BowT/F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin substrate.
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Sequence 33 AA;

ó Gaps ö 100.0%; Score 109; DB 8; Length 33; 100.0%; Pred. No. 2.8e-10; Indels Mismatches ö Conservative Best Local Similarity Matches 22; Conserv Query Match

2 ADSNKTRIDEANQRATKMLGSG 23

AEA14927 standard; peptide; 33 AA. AEA14927;

14-JUL-2005 (first entry)

Goldfish SNAP-25 substrate BoNT recognition sequence, SEQ ID NO: 37.

Neurotoxin, fluorescence; SNAP-25; botulinum toxin

Carassius auratus

JS2005100973-A1

13-AUG-2004; 2004US-00917844

28-AUG-2001; 2001US-00942098

(ALLR) ALLERGAN SALES INC

Steward LE, Gilmore MA, Aoki KR;

WPI; 2005-365632/37.

Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in treated sample.

Disclosure; SEQ ID NO 37; 97pp; English.

activity of clostridial neurotoxins such as boulinum neurotoxin (BoNT) and tetanus neurotoxin (TeNT). The method involves treating with a sample, in solution phase under conditions suitable for clostridial toxin procease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, syntaxin) comprising fluorescent protein, first partner of affinity present invention relates to a method for determining protease

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IndelB

100.0%; Score 109; DB 9; 100.0%; Pred. No. 2.8e-10; iive 0; Mismatches 0;

Conservative

Similarity

Best Local Sim Matches 22;

Query Match

Length 33;

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The present invention relates to a method for determining protesse activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT) and tetanus neurotoxin (The sample, in solution phase under conditions suitable for clostridial toxin protesse activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, syntaxin) comprising fluorescent protein, first partner of affinity couple and clostridial toxin recognitions sequence comprising cleavage site, contacting treated sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated among a sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated
                                                                                                                                                                            ö
couple and clostridial toxin recognition sequence comprising cleavage site; contacting treated sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated sample. The present sequence is the goldfish SNAP-25 substrate BONT/A, E, C (botulinum neurotoxin serotypes A, E, C) recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in treated sample.
                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
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                                                                                                                                          Score 109; DB 9;
Pred. No. 2.8e-10;
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                                                                                                                                            100.0%;
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                                                                                                                                                            Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                             Sequence 33 AA
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AEA14923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                  Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, SEQ ID NO 38; 97pp; English.
Aoki KR;
                                                                                                                   AEA14928 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-2004; 2004US-00917844.
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilmore MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-365632/37.
                                                                                                                                                                                                                                                                                      Carassius auratus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treated sample.
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AEA14928
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Search completed: April Job time : 124.249 secs

2 ADSNKTRIDEANQRATKMLGSG 23 CHINICIPLE ADSNKTRIDEANQRATKMLGSG 33

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2: /SIDSS/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length	DB	ΩI	Description
	89	100.0	17	9	US-10-980-346B-6	Sequence 6, Appli
8	69	100.0	17	9	US-10-980-346B-37	
m	69	100.0	17	9	US-10-947-071-33	33,
4	68	100.0	17	9	US-10-948-097-33	33,
'n	69	100.0	18	9	US-10-947-071-35	35,
9	68	100.0	18	9	US-10-948-097-35	35,
7	89	100.0	33	9	US-10-947-071-36	36,
80	69	100.0	33	9	US-10-947-071-40	40,
6	89	100.0	33	9	US-10-947-071-41	Sequence 41, Appl
10	69	100.0	33	9	US-10-948-097-36	Sequence 36, Appl
11		100.0	33	9	US-10-948-097-40	40,
12	68	100.0	33	9	US-10-948-097-41	Sequence 41, Appl
13	69	100.0	116	7	US-11-195-098-11	11,
14	68	100.0	203	9	US-10-947-071-4	4
15	69	100.0	203	φ	US-10-948-097-4	Sequence 4, Appli
16	68	100.0	206	9	US-10-947-071-1	'n
17	89	100.0	206	9	US-10-947-071-2	~
18	68	100.0	206	9	US-10-948-097-1	Ļ,
19	68	100.0	206	9	US-10-948-097-2	Sequence 2, Appli
20	68	100.0	206	7	US-11-169-041-225	Sequence 225, App
21	68	100.0	334	9	US-10-947-071-20	20,
22	68	100.0	334	9	US-10-948-097-20	20,
23	65	92.6	17	9	US-10-980-346B-38	Sequence 38, Appl
24	65	92.6	17	9	US-10-947-071-61	61,
25	65	92.6	17	9	US-10-948-097-61	Sequence 61, Appl

Appli	Appli	Appl																	
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Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence
US-10-980-346B-1	US-11-195-098-8	US-10-947-071-30	US-10-948-097-30	US-10-947-071-32	US-10-948-097-32	US-10-947-071-34	US-10-947-071-53	US-10-947-071-55	US-10-947-071-60	US-10-948-097-34	US-10-948-097-53	US-10-948-097-55	US-10-948-097-60	US-10-947-071-54	US-10-947-071-58	US-10-947-071-62	US-10-948-097-54	US-10-948-097-58	US-10-948-097-62
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22	24	13	13	16	16	11	17	17	17	17	11	11	17	11	17	17	17	17	17
95.6	92.6	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	95.6	95.6	95.6	95.6	95.6	97.6
65	65	64	64	64	64	64	64	64	64	64	64	64	64	63	63	63	63	63	63
56	27	28	29	30	31	20	33	34	35	36	37	8	6 6	4	41	4.2	43	44	45

ALIGNMENTS

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APPLICANT: Los Alamos National Laboratory
APPLICANT: Schmidt, Jurgen G., et al.
APPLICANT: Schmidt, Jurgen G., et al.
TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
TITLE OF INVENTION: of Botulinum Neurotoxins
TITLE OF INVENTION: of Botulinum Neurotoxins
TITLE REPERENCE: S-102,313
CURRENT APPLICATION NUMBER: US/10/980,346B
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.2
SEQ ID NO 37
LENGTH: 17
GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Los Alamos National Laboratory
| APPLICANT: Schmidt, Jurgen G., et al.
| TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
| TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
| TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
| TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
| TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
| TITLE OF INVENTION: Associated for Detection and Differentiation
| TITLE OF INVENTION: Associated for Detection and Differentiation
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| TITLE OF INVENTION ASSOCIATED for Detection and Differentiation
| TITLE O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Score 68; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 18
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Publication No. US20060063222A1
GENERAL INFORMATION:
APPLICANT: Verhagen, Marce;
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance;
APPLICANT: Abricant Gilmore, Marcella
APPLICANT: Abricant Gilmore, Marcella
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Pletermining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION UNMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
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Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                             Length 17;
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100.0%; Pred. No. 6.2e-07;
tive 0; Mismatches 0;
                                        100.0%; Score 68; DB 6; I
100.0%; Pred. No. 5.8e-07;
ative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                 %3-10-947-071-35

Sequence 35, Application US/10947071

Publication No. US20060063221A1

GENERAL INFORMATION:
                                                                                                                                            2 TRIDEANORATKML 15
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                                          Query Match
Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conservative
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US-10-948-097-35
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US-10-948-097-33
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                                             FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
OTHER INFORMATION: Neurotoxin (BoNI)
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US-10-947-071-33

US-10-947-071-33

Sequence 33, Application US/10947071

Publication No. US20060063221A1

Sequence 33, Application World Sequence 31, Application World Sequence 31, Applicant: Walliams, Dudley J.

APPLICANT: Welman, Marcella

APPLICANT: Verhagen, Marce

APPLICANT: Verhagen, Marc

APPLICANT: Verhagen, Marc

APPLICANT: Verhagen, Marc

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

FILE REFERENCE: 668072-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT PILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SEQ ID NO 33

LEMOTH: 17
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Sequence 33, Application US/10948097
Sequence 33, Application No. US20060063222A1
GENERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Applicant Application Assays For TITLE OF INVENTION: Determining Clostridial Toxin Activity FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 17
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                                                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                 ; LOCATION: (1). [(17); OTHER INFORMATION: amide bound at one end of the peptide US-10-980-346B-37
                                                                                                                                                                                                                                                                Query Match
100.0%; Score 68; DB 6; L
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 14; Conservative 0; Mismatches 0;
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 14; Conservative
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CRGANISM: Homo sapiens
US-10-947-071-33
                                                                                                                   FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(17)
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ORGANISM: Homo sapiens
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Gaps
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                    APPLICANT: Verhagen, Marc
APPLICANT: Aoki, Kei Roger
TITLE OF TITLE OF THE AOKI, Kei Roger
TITLE OF THE CONTINUE Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 41
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Greated, Marcella
APPLICANT: Greward, Lance
APPLICANT: Greward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT PAPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 36
LENGTH: 33
LENGTH: 33
TYPE: RR
CREANISM: Mus musculus
US-10-948-097-36
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APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITHE OF INVENTION: Pluorescence Polarization Assays For
TITHE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION UNDBER: US/10/948,097
CURRENT FILING DATE: 2044-09-22
NUMBER OF SEQ ID NOS: 96
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100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-948-097-36

; Sequence 36, Application US/10948097

; Publication No. US20060063222A1

; GRNERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TRIDEANORATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 TRIDEANORATKML 30
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Steward, Lance
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Best Local Similarity
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APPLICANT:
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                                                                                             Squence 36, Application US/10947071

Fublication No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Lanchanide-Based Substrates and Methods

TITLE OF INVENTION: Lanchanide-Based Substrates and Methods

TITLE OF INVENTION: Lanchanide-Based Substrates and Methods

TITLE OF INVENTION: For Determining Clostridial Toxin Activity

FILE REFERENCE: 66892-043

CURRENT APPLICATION NUMBER: US/10/947,071

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SQOTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36

IRNGTH: 33

TYPE: PRT
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APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
FILE REFREENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 33
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100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 33;
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100.0%; Pred. No. 1.3e-06;
Ative 0; Mismatches 0; Indels
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US-10-947-071-40
; Sequence 40, Application US/10947071
; Sequence 10, Application US/10947071
; GENERAL INFORMATION:

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Query Match 100. Best Local Similarity 100. Matches 14; Conservative

) ORGANISM: Mus musculus US-10-947-071-36

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RESULT 9
US-10-947-071-41
Sequence 41, Application US/10947071
Publication No. US20060063221A1
GENERAL INFORMATION:

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TYPE: PRT ORGANISM: Carassius auratus

US-10-947-071-40

APPLICANT: Williams, Dudley J. APPLICANT: Gilmore, Marcella

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OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
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; Sequence 4, Application US/2060063222A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Dudley J.
    APPLICANT: Williams, Dudley J.
    APPLICANT: Steward, Lance
    APPLICANT: Acki, Kei Roger
    TITLE OF INVENTION: Pluorescence Polarization Assays For
    TITLE OF INVENTION: Determining Clostridial Toxin Activity
    FILE REFERENCE: 66872-040
    CURRENT APPLICATION NUMBER: US/10/948,097
    CURRENT FILING DATE: 2004-09-22
    NUMBER OF SEQ ID NOS: 96
    SOFTWARE: FastSEQ for Windows Version 4.0
    ; ROG ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10947071
Publication No. US20060063221A1
Publication No. US20060063221A1
Publication No. US20060063221A1
SEGRERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Lanchenide-Based Substrates and Methods
TITLE OF INVENTION: For Determining Clostridial Toxin Activity
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                                                                                                                                                                                                                Query Match
100.0%; Score 68; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
                          NAME/KEY: misc_feature; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-11-195-098-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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TYPE: PRT
ORGANISM: Carassius auratus
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Best Local Similarity
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TYPE: PRT
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Sequence 11, Application US/11195098
| Publication No. US20050287622A1
| Sequence 11, Application US/11195098
| Publication No. US20050287622A1
| GENERAL INFORMATION:
| APPLICANT: Schmidt, James J.
| APPLICANT: Schmidt, James J.
| APPLICANT: Stafford, Robert G.
| TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid TITLE OF INVENTION: Nouncoxins |
| TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid TITLE OF INVENTION: Nouncoxins |
| TITLE OF INVENTION: Nouncoxins |
| TITLE OF INVENTION: Nouncoxins |
| FRICK APPLICATION NUMBER: US/10/802,574 |
| PRIOR FILING DATE: 2004-03-17 |
| PRIOR FILING DATE: 2000-09-25 |
| PRIOR FILING DATE: 2001-09-25 |
| NUMBER OF SEQ ID NOS: 12 |
| SEQ ID NO 11 |
| LEWITH: 116 |
| LEWITH: 116 |
| TYPE: PRT |
| PRIOR ATTIFICIAL Sequence |
| FEATURE: PRT |
| PRIOR ATTIFICIAL SEQUENCE |
| PRIOR ATTIFICATION NUMBER OF SEQ ID NO 11 |
| LEWITH: 116 |
| TYPE: PRT |
| PRIOR ATTIFICATION NUMBER OF SEQ ID NO 11 |
| LEWITH: 116 |
| FEATURE: PRT |
| PRIOR ATTIFICIAL SEQUENCE |
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US-10-948-097-41

Sequence 41, Application US/10948097

Publication No. US2006005322A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc.

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Aoki, Kei Rogen

TITLE OF INVENTION: Determining Clostridial Toxin Activity

TITLE OF INVENTION: Determining Clostridial Toxin Activity

TITLE OF INVENTION: 1004-09-22

CURRENT FILING DATE: 2004-09-22

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 41

LENGTH: 33

TYPE: DPT
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100.0%; Score 68; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          ; Score 68; DB 6; ]; Pred. No. 1.3e-06; 0; Mismatches 0;
      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40 LENGTH: 33
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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                                                                                                   ; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40
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US-10-948-097-41
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Matches 14; Conservative 0; Mismatches 0; Indels

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                                                                                                                                  April 3, 2006, 15:46:49; Search time 68.844 Seconds (without alignments) 97.107 Million cell updates/sec
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Sequence 30, N
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Sequence 2, Al
Sequence 52, N
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-942-028-94

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US-09-942-098-94

US-09-942-098-30

US-10-261-161-52

US-10-261-161-68

US-10-261-161-68

US-10-917-844-30

US-09-942-098-32

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US-09-942-024-88
US-09-942-098-88
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Maximum DB seq length: 200000000
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68
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Sequence 4, Appli
Sequence 112, App
Sequence 11, Appl
Sequence 11, Appl
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OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 68; DB 3; Length 16; 100.0%; Pred. No. 3.3e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Acki, Kei Roger.
APPLICANT: Acki, Kei Roger.
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803;
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 91
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Steward, Lance E. APPLICANT: Fernandez-Balas, Ester APPLICANT: APKI, Kei ROgla. APPLICANT: APKI, Kei ROglar IITLE OF INVENTION: Fret Protease Assays For Botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1 -
OTHER INFORMATION: Xaa=fluorescein-modified lysine
US-09-942-024-90
US-09-942-098-90
US-09-942-024-33
US-09-942-024-37
US-09-942-024-38
US-09-942-098-33
US-09-942-098-33
US-09-942-098-33
US-10-261-161-55
US-10-261-161-59
US-10-261-161-59
US-10-917-844-33
US-10-917-844-34
US-10-917-844-38
US-10-917-844-34
US-10-917-844-38
                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 94, Application US/09942024; Publication No. US20030143650A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 91, Application US/09942024; Publication No. US20030143650A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TRIDEANORATKML 15
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Best Local Similarity 100.
Matches 14; Conservative
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PEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
---hos 14; Conservative
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                      JS-09-942-098-94
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NAME/KEY: MOD_RES
LOCATION: LOCATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 16
LOCATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-42-098-91

Sequence 91, Application US/09942098

Publication No. US20030143651A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802

CURRENT APPLICANTE: P-AR 4802

CURRENT APPLICANTON: Toxins

FILE REFERENCE: P-AR 4802

CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 91

LENGTHAR: P-BELSEQ for Windows Version 4.0

SEQ ID NO 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 68; DB 3; Length 16; 100.0%; Pred. No. 3.3e-05; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 68; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                        PEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEY: WOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa-DABCYL modified lysine
NAME/KEY: WOD_RES
LOCATION: 16
OTHER INFORMATION: Xaa=EDANS modified glutamate
NAME/KEY: AMIDATION:
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FRASERO for Windows Version 4.0
SOFTWARE: 16
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CTHER INFORMATION: at the C-terminal US-09-942-098-91
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OTHER INFORMATION: at the C-terminal
                                                                                                                                                                    TYPB: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 14; Conservative
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100.0%; Score 60; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 94, Application US/09942098
| Sequence 94, Application US/09942098
| Publication No. US20030143651A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E. APPLICANT: Ferrandez-Salas, Ester APPLICANT: Aoki, Kei Roger TITLE OF INVENTION: Text Protease Assays For Clostridial TITLE OF INVENTION: Text WOODS FILE REFERENCE: P-AR 4802
| CURRENT PILING DATE: 2001-08-28 | CURRENT PILING DATE: 2001-08-28 | NUMBER OF SEC ID NOS: 96 | SOFTWARE: FastSEQ for Windows Version 4.0 | ENGREPHENCE: 16 | 
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| Sequence 30, Application US/09942024
| Publication No. US20030143650A1
| Publication No. US20030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E.
| APPLICANT: Pernander-Salas, Ester
| APPLICANT: APPLICANT: ACAI, Kel ROGEr
| TITLE OF INVENTION: Fret Protease Assays For Botulinum
| TITLE OF INVENTION: Serotype A/E Toxins
| FILE REFERENCE: P-AR 4803
| CURRENT APPLICATION NUMBER: US/09/942,024
| CURRENT FILING DATE: 2001-08-28
| NUMBER OF SEQ ID NOS: 96
| SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
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OTHER INFORMATION: Xaa=EDANS modified glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa-DABCYL modified lysine NAME/KEY: MOD_RES
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US-09-942-098-30

RESULT

Gaps

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Sequence 68, Application US/10261161

Sequence 68, Application US/20270A1

Sequence 68, Application No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Call-Based Fluorescence Resonance Energy

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSEQ for Windows Version 4.0

TENGTH: 17
                                            GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 17
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Publication No. US20050100973A1

Publication No. US20050100973A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Gilmore, Marcella A.

APPLICANT: Aoki, Kei R.

APPLICANT: Aoki, Kei R.

TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay

TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity

FILE REFERENCE: 66872-044

CURRENT APPLICATION NUMBER: US/10/917,844

CURRENT FILING DATE: 2004-08-13

PRIOR APPLICATION NUMBER: US 09/942,098
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100.0%; Score 68; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 68; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 14; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                  Publication No. US20040072270Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TRIDEANQRATKML 15
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CRGANISM: Homo sapiens
US-10-261-161-52
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US-10-261-161-68
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Sequence 2, Application US/10011588

Publication No. US20020168727A1

CENNERAL INFORMATION:
APPLICANT: Smith, Leonard
APPLICANT: Jensen, Melody
TITLE OF INVENTION: RESEARCH AND LIGHT CHAIN FUSION PROTEINS
TITLE OF INVENTION: RESEARCH AND LIGHT CHAIN FUSION PROTEINS
TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
TITLE OF INVENTION: NUMBER: US/10/011,588
CURRENT APPLICATION NUMBER: US/10/186
PRIOR PILING DATE: 2001-07-20
PRIOR PILING DATE: 2000-07-06
PRIOR PILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2

LUMBER OF SECTION NOTE AND ADDRIVED AND ADDRIVED
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; Sequence 30, Application US/09942098;
; Publication No. US2030143651A1
; GENERAL INFORMATION:
    APPLICANT: Steward, Lance E.
    APPLICANT: Pernandez-Salas, Ester
    APPLICANT: Aoki, Kei Roger
    TITLE OF INVENTION: Fret Protease Assays For Clostridial
    TITLE OF INVENTION: Toxins
    TILE REFERENCE: P-AR 4802
    CURRENT APPLICATION NUMBER: US/09/942,098
    CURRENT FILING DATE: 2001-08-28
    NUMBER OF SEQ ID NOS: 96
    SOFTWARE: PastSEQ for Windows Version 4.0
    SEQ ID NO 30
    LEMACTU: 17
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Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.5e-05;
tive 0; Mismatches 0;
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LOCATION: (0)...(0)
OTHER INFORMATION: Residues 187-203 of SNAP-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-261-161-52
; Sequence 52, Application US/10261161
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30
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Gaps

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2 TRIDEANQRATKML 15
                                          5 TRIDEANORATKML 18
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US-10-261-161-54
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ORGANISM: Homo sapiens
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US-09-942-024-85
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US-10-917-844-32
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LENGTH: 18
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LENGTH: 18
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; Sequence 32, Application US/09942098
; Publication No. US20030143651A1
; Deblication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Acki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: For Decrease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ 1D NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3.9
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 68; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 3.8e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            Length 17;
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publication No. Application US/09942024

publication No. Application US/09942024

publication No. Application US/09942024

general INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Sallas, Ester
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serctype A/F Toxins
FILE REFERENCE: P-AR 4803
CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 18
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Score 68; DB 3; L
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0;
                   NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
TYPE: PRT
  PRIOR FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                  4 TRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRIDEANORATEML 18
                                                                                                                                                                                                                                                                                 2 TRIDEANQRATKML 15
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                                                                                                                              ; ORGANISM: Homo sapiens
US-10-917-844-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-09-942-024-32
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kai Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/B Toxins
FILE REFERENCE: P-AR 4803
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT APPLICATION NUMBER: US/09/942,024
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 85
LENGTH: 19
FRAURE: PRT
ORGANISM: Artificial Sequence
FRAURE: OTHER INFORMATION: synthetic construct
OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 1
COTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: MAIDATION
COTHER INFORMATION: At the C-terminal
US-09-942-024-85
OTHER INFORMATION: at the C-terminal
US-09-942-024-85
Matches 14; Corservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: April 3, 2006, 15:57:05 Job time : 68.844 secs

2 TRIDEANORATKML 15

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Sequence 1, Appli
Sequence 37, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appli
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Sequence 2, Appli
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Sequence 4, Appli
Sequence 4, Appli
Sequence 31, Appli
Sequence 3, Appli
Sequence 25, Appli
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/F_COMB.pep:*

(cgn2_6/ptodata/1/iaa/F_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-743-894B-1

US-08-819-286-9

US-08-819-286-4

US-08-19-286-4

US-08-19-286-4

US-09-15-960-10

US-09-534-572-10

US-09-534-572-10

US-09-19-286-11

US-09-19-286-11

US-09-19-286-11

US-08-143-894B-2

US-08-743-894B-3

US-08-743-894B-3

US-08-743-894B-37

US-08-743-894B-37

US-08-743-894B-27

US-08-743-894B-29

US-08-743-894B-25

US-08-743-894B-25
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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68
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Match Length DB
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Perfect score:
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							ALI	ALIGNMENTS	NTS									
	що	14B-1	icatio	'SD uz	,087	4389	4 8											
	POTENT NO. 595599; GENERAL INFORMATION: APPLICANT: James J. Schmidt	S9656 INFORM	TION:	r. Sch	himi	ш												
	APPLICANT: Karen A. Be TITLE OF INVENTION: A. NUMBER OF SEQUENCES:	NT: I	Caren / INTION: QUENCES	A. Bog ABB 3: 56	atia say S	n for	the	Pro	teoly	tic	Acti	Bostian Assay for the Proteolytic Activity o 56	of Ser	roty	Se A	Serotype A Neurotoxin	oxin	frc
	CORRESI CORRESI DADDRI STREE	RRESPONDENCE ADDRESS: ADDRESSE: MCMM-JA Attn:John Moran-Patent Atty STREET: USA MRMC - 504 Scott Street	NCMR-	(BSS: - JA A1	ttn: 34 S	Johr	Mo St.	ran-	Paten	it At	:ty							
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	ZIP. 21702-5012	2170; SR REAL	-5012	ORM:	-													
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	FILIN	NG DAT	ION:	435	2695	embe	3r 6	13	96									
	; PRIOR ; APPL:	ICATION NG DATE	NUMBI	88:														
	, ATTORNI , NAME	EY/AGE	AT INF	ORMAT Har	ION:	616												
	REFEI	RENCE/	ATION	NUMB	ER: /	NO.												
	TELEFACINES (301) 619-7714 ; INFORMATION FOR SEQ ID NO: 1: CEPUTANCE CHARACTERISTICS:	FAX: FAX: ION FO	(301) R SEQ	619-7 ED NO	714	2 3												
	LENGTH:	LENGTH: 17 TYPE: amino STRANDEDNESS TOPOLOGY: L	: 17 amino acids amino acid sequence EDNESS: Single GY: Linear	d sed ingle	des	ø												
_	Query Match Best Local Matches 1	Simi 4;	100 Similarity 100 14; Conservative	10 10 vativ	100.0%; 100.0%; tive		Score Pred. ; Mism	:e 68; 1. No. :вщатсh	ore 68; Di ed. No. 6. Mismatches	DB 1; 6.7e-00	6; 6; 6;	Length 17 Indels	0		Gaps	0;		
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Sequence 8, Application US/08819286
Sequence 8, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DEPTIDE INHIBITORS OF
TITLE OF INVENTION: DEPTIDE OF THE OFFICE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OF THE OFFICE OF
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100.0%; Score 68; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                 CLASSIPTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: TAYLOR. Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECHOMONICATION INFORMATION:
TELECHONE 619/678-5070
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,842
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TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TRIDEANORATKML 15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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STATE: CA
COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                              FILING DATE:
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US-08-819-286-8
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                                                                                                                            Sequence 37, Application US/08743894B

Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: 56
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: MCMR-JA Attn.John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
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Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPFIDE INHIBITORS OF
TITLE OF INVENTION: NEUFOTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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100.0%; Score 68; DB 1; I
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: FURNIERAL STATES
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743, 894B
FILLING DATE: No. 5965699ember 6, 1996
CLASSIFICATION 1435
PRIOR APPLICATION UNBER: 33,616
REPLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 31,616
REGINALION FOR SEQ ID NO: 37;
SECURIOR CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Gaps

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APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Ouinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler C.TTW.
CTTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserva
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STATE:
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Patent No. 6159074

GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEIROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Alchardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
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100.0%; Pred. No. 1.6e-05;
                                                                                                                                            100.0%; Score 68; DB 2; I
100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 10, Application US/08760001
; Patent No. 5962637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REPERBOCOLOCKET NUMBER: 0734;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
                                         TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-8
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STRANDEDNESS: not
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US-08-760-001-10
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GENERAL INFORMATION:

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Patent No. 6043042

GENERAL INFORMATION:
APPLICANT: Alone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Weshington
CENTY: Weshington
CENTY: Weshington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 68; DB 1; Length 70; 100.0%; Pred. No. 3.4e-05;
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3: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
1100 New York Ave., N.W., Suite 600
                                                                                                                    CUNNIKY: USA

ZIP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
CLASSIFICATION NUMBER: B/08/760,001
FILING DATE: Herewith
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-010N-1995
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND' RODERT W.
REGISTRATION NUMBER: 32.893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELEBEHONE: 202-317.2500
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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US-09-534-572-10

Sequence 10, Application US/09534572

Sequence 10, Application US/09534572

Patent No. 6337386

APPLICANT: Shone, Clifford C.
APPLICANT: Halls, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 68; DB 2; Length 70; 100.0%; Pred. No. 3.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
                                                                                                                         FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Bemond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-260
TELEPAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TRIDEANQRATKML 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OP INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OP INVENTION: Heart Coxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US 69/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR PILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT
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Sequence 18, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 68; DB 2; Length 116; 100.0%; Pred. No. 6e-05;
                                                                                                                                                                                                                                    Query Match
100.0%; Score 68; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-09-962-360B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
TELEPAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 aming acids
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-10
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Mon Apr

not relevant

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STRANDEDNESS:
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Patent No. 6169074

GENERAL INFORMATION:
TITLE OF INVENTION: NEUTOTRANSMITTER SECRETION BY NEURONAL CELLS
TITLE OF INVENTION: NEUTOTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Johla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:
CLASSIFICATION NUMBER: US/08/393,985
ATTORNEY/AGENT INFORMATION:
NAME: Sholts, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 36,600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 anino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 68; DB 1; L
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 860/013,599
FILING DATE: 18-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: TAYLOR, Stacy L.
REGISTATION NUMBER: 34,842
REPERRORE/DOCKET NUMBER: 07349/00500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Sequence 6311, Application US/09949016

Sequence 6311, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL1307

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOOTHARRE: FEASESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 6311

LENGTH: 206
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FARENTAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILLING DATE: 2000-04-14

PRIOR PILLING DATE: 2000-10-20

PRIOR PILLING DATE: 2000-10-03

PRIOR PILLING DATE: 2000-10-03

PRIOR FILLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FBELSEQ for Mindows Version 4.0

LENGTH: 219
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                                                                                                100.0%; Score 68; DB 2; Length 206; 100.0%; Pred. No. 0.00012; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 68; DB 2; Length 20 Best Local Similarity 100.0%; Pred. No. 0.00012; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10671, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                  2 TRIDEANQRATKML 15
                                                                                                      Query Match
Best Local Similarity 100.0
Matches 14; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-819-286-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-10671
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US-09-949-016-6311
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Score 65; DB 1; Length 17;
Pred. No. 2.4e-05;
                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Job time : 12.7706 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.6%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                               STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TRIDEANQRATKML 15
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Patent No. 5865699

GENERAL INFORMATION:
APPLICANT: Karen A. Bostian
TITLE OF INVENTION:
APPLICANT: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES:
ADDRESSES:
ADDRESSES:
ANDERSON MARTIAND
COUNTRY: USA
CONPUTER: REALBALE FORM:
MICHORY PEE: Florgy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macin
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US-08-743-894B-18
US-08-743-894B-18
i Sequence 18, Application US/08743894B
i Patent No. 5965699
i GRNERAL INFORMATION:
APPLICANT: Waren A. Bostian
ITILE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fir NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
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                                                                     Gaps
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   Length 219;
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                                                               0; Indels
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USA MRMC - 504 Scott Street
; Score 68; DB 2; I
; Pred. No. 0.00012;
0; Mismatches 0;
      100.0%;
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TYPE: amino acid sequence
STRANDEDNESS: Single
                                                                                                                                                                    203 TRIDEANORATKML 216
                                                                                                                              2 TRIDEANORATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TRIDEANORATKML 15
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Matches 13; Conservative
   Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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Gaps

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0; Indels

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 3, 2006, 15:27:42; Search time 82.4954 Seconds (without alignments) 136.837 Million cell updates/sec

Title: US-09-942-098-91
Perfect score: 68
Sequence: 1 XTRIDEANQRATEMLX 16

Sequence: 1 XTRIDEANQRATKWLX 16 Scoring table: BLOSUM62

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum DB seq Lengtn: Z000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Listing first 45 sum:
UniProt 05.80:*

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Descripcion	-	tetraoc			60		4	-					0	7 maca	mus	pan tro	ratto	homo	homo	pong		Q5r690 pongo pygma	1 obuod	Q4r4u6	Q4v809	06p317	Q5r505]		066id7	Q4v9b7 brachyda	000
SUMMERTES	Ş	ai		Q4S8B5_TETNG	Q9GM34 MACFA	Q6PC84 BRARE	SN25B CARAU	093579 BRARE	Q6PC54_BRARE	SN25A CARAU	Q705J6 LATJA	Q5TZ66_BRARE	QSTZ65 BRARE	SNP25 CHICK	SNP25 HUMAN	SNP25 MACMU	SNP25 MOUSE	SNP25_PANTR	SNP25 RAT	Q53EM2 HUMAN	QSUOB5 HUMAN	QSNVG5 PONPY	Q5NVK3 PONPY	Q5R690 PONPY	QSR6U7_PONPY	Q4R4U6_MACFA	Q4VS09 CARAU	Q6P3L7_BRARE	Q5R505 PONPY	Q7ZVE4 BRARE	Q66ID7_BRARE	Q4V9B7_BRARE	A TINETY AND A CO.
	6	BB :	~	~	~	N	н	~	N	Н	~	7	7	٦	Н	ч	н	-	٦	~	~	~	7	7	7			~		7	~	~	c
		Match Length	124	134	143	198	203	203	203	204	204	204	204	206	206	206	206	206	206	206	206	206	206	206	206	206	236	204	206	214	137	186	000
	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.1	89.7	80.9	79.4	79.4	,
		Score	89	68	68	89	89	68	68	99	68	89	89	68	69	68	69	99	68	68	68	9	68	68	69	68	68	64	61	55	54	54	•
	Result	No.	1	7	М	4	ហ	φ	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	;

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xenopus brachyda brachyda torpedo loligo p tetraode xenopus lymnaea pseudomc pseudomc pseudomc pseudomc pseudomc pseudomc pseudomc pseudomc pseudomc pseudomc	niformes; .CO;2-Z; ait J.H., h: e locus in	0; Gaps	
Q8axm1 Q8axm2 Q4ayb6 P36976 P36976 Q81187 Q85430 Q85430 Q85440 Q85440 Q85440 Q85440 P11221	Euteleo 1; Cypri JWRl>3.3 JWRl>3.3 ses of on A.	CRC64; Length 124; Indels	
AAN MUKHUJONZ H	ted) sequence update) annotation update) annotation update) annotation update) anio rerio) aniata; Vertebrata; E eostei; Ostariophysi; 1201)54:5<563::AID-JN erg C., Gates M., Pos protein Snap25 in ze groups suggests loss groups suggests loss 8). RNA. factor activity; IEA. factor activity; IEA. transcription, DNA-de	D958C B 2; 0004;	
Q8AXM1_XENLA Q8AXM2_XENLA Q4V9B6_BRARE SNP25_TORMA Q8T354_LOLPE Q4REP6_TETNG Q8J137_XENLA Q869G6_LYMST Q85431_9PSED Q85431_9PSED Q85431_9PSED Q81389_HIRME Q8NCR8_HUMAN QRNCR8_HUMAN QRNCR8_HUMAN QRNCR8_HUMAN	PRT; tr sequent annot be be be be be be ground be be ground be	; SOE27DBDB33 Score 68; D Pred. No. 0. 0; Mismatches	
0000000000000	28, (28), (28), (3	13616 MW 100.0%; 100.0%; tive	15 121
206 200 210 210 210 220 83 83 83 83 83 83 83 83 83 83	MINARY, MILTEL. (MI	8	
44446000000000000000000000000000000000	PRY BRAKE 093578 BRAKE PRELIMINARY; 093578 BRAKE PRELIMINARY; 093578 BRAKE PRELIMINARY; 01-NOV-1998 (TrEMBLrel. 08, Last ol-NOV-1998 (TrEMBLrel. 26, Last ol-NOV-1998 (TrEMBLrel. 06, Last ol-NOV-1998) (Tremblary ol-NOV-1998) (Tremblary ol-NOV-1998) (Tremblare, Danio. NCBI_TAXID=7955; [1] NUCLECTIDE SEQUENCE. MEDIINE=99057281; Pubmed=9843147; DOI=10.1002/(SICI)1097-4547(19981) Risinger C., Salaneck E., Soderbe Larhammar D.; Salaneck E., Soderbe Comparison of paralogous linkage the mammalian lineage."; Cloning of two loci for synapse occuparison of paralogous linkage the mammalian lineage."; J. Neurosci. Ree. 54:563-573(1998 EMBL; AF091593; AAC64289.1; -; mR HSSP; QR1384; 114A. SKR; O93578; Pregallation of EGO; GO:0019717; C:Synaptosome; IEGO; GO:0003700; F:transcription for InterPro: IPRO002197; HTH FS. PROMINTS; PRO1059; PRO1059; HTHFS. SMART; SMO0397; L'SNARE; I. PROSITE; PS50192; T_SNARE; I. NON WERE	T T	TRIDEANQRATKML TRIDEANQRATKML
N N N N N N A A A A A A A A A A A A A W W O N N N W W G G	# BRAKE 093578 BRAKE PRE 093578 BRAKE PRE 01-NOV-1998 (TrE NAR-2004 (TrE CAPTINIDES ACTINIDES ACTINIDES ACTINIDES NOUCLEOUTIDE SEQUE MEDLINE=99057281; 10-NOUCLEOUTIDE SEQUE RESINGER C., Sallarammarian of two Compartison of pa Trandammarian of two Trandammaria	at ch	2 T 108 T
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RESULT 2

us-09-942-098-91.rup

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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Adillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Iutfalla G., Dossat C., Segurens B.,
Dasilya C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J.P., Gouzy J.,
Acruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A. Kellis M., Volff JW., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Schachter P., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E. S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
III hature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain parietal lobe;
Osada M., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                  Tetrandon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea, Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14706, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL: CAAEQ1014706; CAG03117.1; -; Genomic DNA.
SEQUENCE 134 AA; 14682 MW; 09109FP243890A8E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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EMBL; AB049852; BAB16738.1; -; mRNA.
HSSP; Q8T3S4; 1L4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
11-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 AA
                                     134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                            ORFNames=GSTENG00022427001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 TRIDEANORATKML 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TRIDEANQRATKML 15
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Q9GM34;
                             Q4S8B5 TETNG PRELIMINARY;
Q4S8B5;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=99883;
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CENTRAINBUILD SEQUENCE.

STRAINBUILD SEQUENCE.

STRAINBUILD SEQUENCE.

STRAINBUILD SEQUENCE.

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RELLINE STR., Feligold B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S. I., Wang J., Heich F.,

A Distchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rachards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 68; DB 2; Length 143; 100.0%; Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                       GO, GO:0019717; C:synaptosome; IEA.
InterPro; IPR00028; SNAP-25.
InterPro; IPR000727; T:SNARE.
Pfam; PF00315; SNAP-25; 1.
Pfam; PF00315; SNARE; 1.
SWART; SM00397; t. SNARE; 1.
SWORT; SNO0192; T. SNARE; 1.
Hypothetical protein; Synaptosome.
SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGPC84_BRARE PRELIMINARY; PRT; 198 AA.
QGPC84;
QGPC84;
QGPC84.
QGPC84;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ...
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SWR; Q6PC84; 1-77, 123-196.
ZFIN; ZDB-GRNE-986526 468; snap25a.
GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000228; SNAP-25.
InterPro; IPR000727; T_SNARE.
PEam; PP00835; SNARE.
PEam; PP00835; SNARE; 1.
SWART; SW00397; L_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 TRIDEANQRATKML 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TRIDEANORATKWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
SMR; Q9GM34; 68-141
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187 TRIDEANQRATKML 200
2 TRIDEANQRATKML 15
                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                           NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                            Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=snap25b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synaptosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6PC54;
                                                                               BRARE
                                                                                                        093579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Q6PC54_BR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
-1- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                  Gaps
                                                                                                                                                                                                                                                                                         Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prons Pro0835; c.....
Pfam; PF05739; SNARE; 1.
SNARE; 2.
PROSITE; PS50192; T SNARE; 2.
PROSITE; PS50192; T SNARE; 2.
COLLed coil; 01ycoprotein; Multigene family; Repeat; Synaptosome.

t - SNARE coiled-coil homology 1.

t - SNARE coiled-coil homology 2.

t - SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the nerve terminal.
--- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, a granule cells of the cerebellum.
--- SIMILARITY: Belongs to the SNAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 Cys-rich.
77 N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
185 N-linked (GlCNAc. . .) (Potential)
22664 MW; 8DFBBEDBED37D6D7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-34068448; PubMed-8248151;
Risinger C., Larhammar D.;
"Multiple loci for synapse protein SNAP-25 in the tetraploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 68; DB 1; Length 203; 100.0%; Pred. No. 0.00067; tive 0; Mismatches 0; Indels
                                        Length 198;
                                                                  0; Indels
               198 AA; 22209 MW; 8FED5099A00E1EC0 CRC64;
                                       Score 68; DB 2; L
Pred. No. 0.00065;
                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Synaptosomal-associated protein 25B (SNAP-25B)
                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L22976; AAA16538.1; -; mENA.
PIK; 150481. 150481.
HSR; p13795; LSFC.
SMR; P36978; 7-82, 128-201.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; TSNARE.
Pfam; PP008135; SNAP-25; 1.
                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
                                       / Match 100.0%;
Local Similarity 100.0%;
he 14; Conservative 0
                                                                                                                                                                                                                                                                                       Carassius auratus (Goldfish)
                                                                                                                         182 TRIDEANQRATKWL 195
                                                                                                2 TRIDEANORATKML 15
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                            Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 14; Conserv
                                                                                                                                                                                                                                                                             Name=SNAP-B;
                                                                                                                                                                                           <u>S</u>N25B_CARAU
P36978;
     Synaptosome
                                                                                                                                                                                                                                                                                                                                                                                                                                           goldfish.",
Proc. Natl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                   SEQUENCE
                                           Query Match
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                                                                                                                                                                                SN25B CARAU
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Matches
                                                           Best Loc
Matches
                                                                                                                                                                  RESULT 5
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Conservative

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"Cloning of two loci for synapse protein Snap25 in zebrafish: "Cloning of two loci for synapse groups suggests loss of one locus in the mammalian lineage.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                        MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
Riginger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Synaptocome-associated protein 25.2.
Name-snap25b; Synonyms=Snap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 68; DB 2; I
100.0%; Pred. No. 0.00067;
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203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Neurosci. Res. 54:563-573(1998).
ENBL; APO91594, AAC64290.1; -; mRNA.
HSSP; PG091; JJTH.
SMR; O93579; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
GO; GO:019717; C:synaptosome; IEA.
InterPro; IPR00928; SNAP-25.
InterPro; IPR00927; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synaptosome-associated protein 25 b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
PRT;
                                             01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SMART; SW00397; t_SNARE; 2.
PR0571E; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 TRIDEANORATKWL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TRIDEANQRATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFPC54_BRARE PRELIMINARY;
O93579_BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
ses 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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Name=snap-25;
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SEQUENCE
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                                                                       removed.
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J. Usdin T.B., Toshiyuki S., Zarninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Millahy S.J., Richards S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., N. Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Willianon D.K., Muzny D.M., Schevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Robert J.B., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         goldfish.";
Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
-!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the nerve terminal.
--- SIMILARITY: Belongs to the SNAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Risinger C., Larhammar D.; "Multiple loci for synapse protein SNAP-25 in the tetraploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 68; DB 2; Length 203;
; Pred. No. 0.00067;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059469; AHF59469:1; -; mRNA.
SMR; QCPC54; 7-82, 128-201.
ZPIN; ZDB-GENE-980526-392; snap25b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 AA; 22693 MW; 48D7590DD0C1179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
Synaptosomal-associated protein 25A (SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA.
                                                                                                                                                                                                                                                                                                                                         GO; GO:0019717; C:8ynaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94068448; PubMed=8248151;
                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN-Wild-type; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM0397; t_SNARE; 1.
SMART; SM0397; t_SNARE; 2.
SWIBSITE; PSS0192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 TRIDEANORATKML 200
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TRIDEANORATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
18 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=SNAP-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SN25A CARAU
P36977;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synaptosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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C TISSUE=Brain;

A Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJG19993; CAF04071.1; -; mRNA.

R SMR; Q705J6; 7-83, 129-202.

R GO; G0:0003700; F: transcription factor activity; IEA.

R GO; G0:0003700; F: transcription of transcription, DNA-dependent; IEA.

BR InterPro; IPR000928; SNAP-25.

DR Pfam; PF00935; SNAP-25; 1.

DR Pfam; PF00935; SNAP-25; 1.

DR RART; SM00397; t_SNARE; 1.

DR SMART; SM00397; t_SNARE; 2.

DR PROSITE; PS50192; T_SNARE; 2.

DR PROSITE; PS50192; T_SNARE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Butelostemi.
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha; Acanthopterygii, Percomorpha; Perciformes; Percoidei,
                                                                                                                                                   EMBL; L22973; AAA16537.1; -; mRNA.

R HSSP; P1795; INA.

R HSSP; P1795; INA.

R INGEPPO; ISO0480.

R InterPro; IPRO00928; SNAP-25.

R InterPro; IPRO00928; SNAP-25.

R Fam; PF05739; SNARE.

R Fam; PF05739; SNARE; 1.

R PRART; SM00397; t SNARE; 2.

R ROSITE; PS50192; T SNARE; 2.

R POMAIN 19 81 t-SNARE coiled-coil homology 1.

DOMAIN 138 200 t -SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 68; DB 1; Length 204; 100.0%; Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cys-rich.
458BBECFCFC09189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
Synaptosomal-associated protein 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 200 t
85 92 C
204 AA; 22843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Guery Match
Best Local Similarity 100...
Best Anna 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 TRIDEANQRATKML 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q705J6 LATJA PRELIMINARY;
Q705J6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8164;
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Gaps

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Length 204;

us-09-942-098-91.rup

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SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 SUBUNIT: Part of the SNARE core complex binds CPLX1. Interacts with TRIM9, RIMS1 and SYALA. This complex binds CPLX1. Interacts with TRIM9, RIMS1 and SNAP258P. Bindis STABPE. Found in a ternary complex with STX1A ALTERNATIVE PRODUCTS:

Event-Alternative Splicing, Named isoforms=2;

Comment-Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP25 CHICK STANDARD; PRT; 206 AA.
P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 17, Last sequence update)
10-MRY-2005 (Rel. 17, Last anotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated 25 NAP-25) (Synaptosomal-associated 25 NAP-25) (Synaptosomal-associated 25 NAP-25) (Synaptosomal-associated 25 NAP-25) (Synaptosomal-associated 25 NAP-25)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of the chicken gene for SNAP-25 reveals duplicated exon "Structure of the chickens of the protein.";
J. Mol. Biol. 233:67-76(1993).
-!- FUNCTION: L-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=White leghorn; TISSUE-Retina;
MEDLINE=91126080; PubMed=1992470;
Cataicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J., Wilson M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson M.C.;
"Expression of a conserved cell-type-specific protein in nerve terminals coincides with synaptogenesis.";
Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
                                                                                                                                                                                                                                                                           204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B) MEDLINE=93389738; PubMed=8377193;
                                                                                                                                                                                                                                                                                                                      100.0%; Score 68; DB 2; I
100.0%; Pred. No. 0.00067;
tive 0; Mismatches 0;
EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA
                     SMR; Q5TZ65; 7-83, 129-202.
Ensembl; ENSDARG0000000609; Danio rerio.
ZFIN; ZDB-GENE-980526-468; snap25a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
                                                                                           GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Fam; PP05335; SNAP-25; 1.
Fam; PP05739; SNARE; 1.
SMART; SM0397; t_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P60878-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P60878-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 TRIDEANORATKML 201
                                                                                                                                                                                                                                                                                                                                                                                                                         2 TRIDEANQRATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed;
Name=SNAP-25a;
                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Query Match
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SNP25 CHIC
                                                                                                                                                                                                                                                                                                                                                                                Matches
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
8ynaptosomal-associated protein (SNAP).
Name-snap25a; Synonyms-CTTDARP0000005590; ORFNames-DKEYP-8F4.6-002;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Annio rerio).
Brachydanio rerio (Zebrafish) (Annio rerio).
Cyprinidae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Cyprinidae; Danio.
NEL TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                           01-FEB-2005 (TrEWBLrel. 29, Created)
01-FEB-2005 (TrEWBLrel. 29, Last sequence update)
01-FEB-2005 (TrEWBLrel. 29, Last annotation update)
8ynaptosomal-associated protein (SNAP).
Name-snap25a; Synonyms-OTTDARP0000005563; ORFNames-DKEYP-8F4.6-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Cyprinidae; Danio.
NCTI-TAXID=7955;
NCBI_TAXID=7955;
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX465184; CA469032.1; -; Genomic_DNA.
EMBL; BX470246; CAIL21360.1; -; Genomic_DNA.
EMBL; BX470246; CAH69032.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX465184; CAH69031.1; -; Genomic_DNA.
EMBL; BX470246; CAI21359.1; -; Genomic_DNA.
EMBL; BX470246; CAH69031.1; JOINED; Genomic_DNA.
EMBL; BX465184; CAI21359.1; JOINED; Genomic_DNA.
EMBL; BX465184; CAI21359.1; JOINED; Genomic_DNA.
EMBL; BX465184; CAI2359.1; BOINED; Genomic_DNA.
EMBL; GSTZ66; 7-83, 129-202.
ENSEMD1; ENSDARGO000020609; Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOVELL J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            LOVELL U.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
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                                                            204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:019717; C:synaptosome; IEA.
Interpro; IPR000928; SNAP-25.
Interpro; IRR000727; T.SNARE.
Pfam; PP00335; SNAP-25; 1.
SNART; SM0337; K. SNARE; 1.
SNART; SM0337; L. SNARE; 2.
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                                                            PRT;
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QSTZ65;
                                                            QSTZ66_BRARE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Donaldson S.;
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SEQUENCE Query Match

Best Loca Matches

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Lovell J

RESULT 11

OGSTZGE BRE

OGSTZGE

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DT 01-FE

DT 01-FE

DT 01-FE

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NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rogers J.;
  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP25 HUMAN STANDARD; PRT; 206 AA.
P60880; P13795; P36574; P70559; Q8IXK3; Q96FM2; Q9BR45;
01-JAN.1990 (Rel. 13, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated brotein) (Super protein) (Super Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphoserine (By similarity).
ERIEEGMDQINKDMKEAEKNLTDLGKFCGLCV -> DRVI
GWNHINQDMKEAEKNLKDLGKCCGLFI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cys-rich.
Cleavage (by BONT/E) (By similarity).
Phosphothreonine (By similarity).
                         -1- PTM: Palmitoylated (By similarity).
-1- SIMILARITY: Belongs to the SNAP-25 family.
-1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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DOMAIN 19 81 t-SNARE coiled-coil homology 1.

T-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 68; DB 1; Length 206; 100.0%; Pred. No. 0.00068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00397; t SNARE; 2.
PROSITE; PS50192; T SNARE; 2.
Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                AAA49070.1; JOINED; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAA49071.1; -; Genomic_DNA. |
| AAA49071.1; JOINED; Genomic_DNA. |
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                                                                                                                                                                                                                                                                       EMBL; M57957; AAA49072.1; -; mRNA.
EMBL; L09253; AAA49070.1; -; Genomic_DNA.
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InterPro, IPR000727; T_SNARE.
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SMR; P60878; 7-83, 131-204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
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     Sequence=VSP 010018;
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L09259; F
L09252; F
L09258; F
L09250; F
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L09254;
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MOD_RES
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                                                                                                                                                                                                                               removed.
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EMBL;
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EMBL;
EMBL;
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RRP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA MININE-21638749; PubMed=1180052; DOI=10.1038/414865a;

Doloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Deloukas P., Batches K.N., Beard L.M., Beare D.M.,

Ra Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burill W.D., Butler A.P., Carder C., Carter N.P.,

Choley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA MINE S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

Syluc C.D., Smith M.L., Soctt C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,

Mitchead S.L., Whittaker P., Willey D.L., Milliams L., Williams S.A.,

Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitcher J. Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A pother D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boniffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skeletal muscle;
MEDLINE=96332494; PubMed=8760387;
Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
Grugovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ward C.W.;
"Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
Biochem. J. 317:945-954 (1996).
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TISSUE=Brain;
MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
Bark I.C., Wilson M.C.;
                                                                                                                                                                                                                                                                                                                                                                                IISSUE=Brain;
MEDLINE=9433829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2;
                                                                                                                "Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25."; Gene 139:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao N., Hashida H., Takahashi N., Sakaki Y.; "Cloning and sequence analysis of the human SNAP25 CDNA."; Gene 145:313-314(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                  [2] NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A).
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          EMBL;
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Best SNP25 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX WITH STXIA, CPLX1 AND VAMP2, AND NWR ANALYSIS.

MEDLINE-21822661, PubMed=11832227, DOI=10.1016/S0896-6273 (02) 00583-4; ACHON X., Tomchick D.R., Kovrigin B., Arac D., Machius M., Suedhof T.C., Rizo J.;

Three-dimensional structure of the complexin/SNARE complex.";

Neuron 33:397-409(2002).

L. FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the proteins involved in vesicle docking and membrane fusion.

PYMADTION: proteins involved in vesicle docking and membrane fusion.

STUBUNIT: Part of the SNARE core complex containing SNARES.

-I- SUBUNIT: Part of the SNARE CPLX1. Interacts with TRIM9, RIMS1, SNARESERP and HGS. Binds STRXIA in a ternary complex with runnary complex with the symbol of the symbo Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human 94 Event=Alternative splicing, Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to and differ only in 9 positions out of 39; MIM, 600322; -.
GO, GO.0007269; P:neurotransmitter secretion; NAS.
GO, GO:0001269; P:neurotransmitter uptake; NAS.
GO, GO:0001504; P:neurotransmitter uptake; NAS.
GO, GO:0007268; P:synaptic transmission; NAS.
GO, GO:0016081; P:synaptic transmission; NAS.
GO, GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE. -!- PTM: Palmitoylated (By similarity).
-!- SIMILARITY: Belongs to the SNAP-25 family.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains. Isold=P60880-2, P13795-2; Sequence=VSP 006186; Sequence=VSP 006186; TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, granule cells of the cerebellum. QBIUH5:HIP14; NDExp=1; IntAct=EBI-524785, EBI-524753; ALTERNATIVE PRODUCTS: Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) EMBL, AL023913; CAC34534.1; -; Genomic_DNA.
EMBL; AL023913; CAC34535.1; -; Genomic_DNA.
EMBL; AL023913; CAD5158.1; -; Genomic_DNA.
EMBL; AL023913; CAD5158.1; -; Genomic_DNA.
EMBL; AL023913; CAB42860.1; -; Genomic_DNA.
EMBL; BC010647; AAH10647.1; -; mENA.
PIR; I53735; I57823; I67823; I67823; I67823; I67823; I67823; I67823; EBB; IXIL; X-ray; C=11-80, D=141-203.
PDB; IXIG; X-ray; E=146-204.
SWR; P60880; 7-83, 131-204. IntAct; P60880; -. Ensembl; ENSG00000132639; Homo sapiens EMBL; L19760; AAC37545.1; -; mRNA. EMBL; L19761; AAC37546.1; -; mRNA. EMBL; D21267; BAA22370.1; -; mRNA. IsoId=P60880-1, P13795-1; and mouse cDNA sequences."; HGNC; HGNC:11132; SNAP25.
H-InvDB; HIX0015639; -.
MIM; 600322; -.
GO; GO:0007269; P:neurotrai GO; GO:0001504; P:neurotrai GO; GO:0001504; P:neurotrai GO; GO:0050796; P:regulatic GO; GO:007268; P:synaptic Sequence=Displayed; Name=SNAP-25a; Name=SNAP-25b INTERACTION:

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                              Cys-rich.
Cleavage (by BONT/E).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
ERIEEGMOQINKDMKEAEKNLTDLGKFCGLCV -> DRVEE
GMNHINQDMKEAEKNLKDLGKFCGLFI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP25 MACMU STANDARD; PRT; 206 AA. P60977; P13795; P36974; P70559; Q8IXK3; Q96FM2; Q9BR45; D1-3M-1990 (Rel. 13, Created) O1-7EB-1991 (Rel. 17, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated

    Fimilarity).
    SUBDIAT: Part of the SNARE core complex containing SNAP25, VAMP2 and STX1A. This complex binds CPLXI. Interacts with TRIM9, RIM81, SNAP2SBP and HGS. Binds STXBP6. Found in a ternary complex with STX1A and VAMP8 (By similarity).
    PIT: Palmitoylated (By similarity).
    SIMILARITY: Belongs to the SNAP-25 family.
    SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

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Jensen M.J., Smith L.A.;
Jensen M.J., Smith L.A.;
Jensen M.J., Smith L.A.;
Jensen M.J., Smith L.A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: t-SNARE involved in the molecular regulation of
neurorizansmitter release. May play an important role in the
synaptic function of specific neuronal systems. Associates with
proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNABE: 1.
SMAST; SMOA397; L_SNABE: 2.
PROSITE; PS50192; T_SNARE; 2.
3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
                                                                                                                                  Palmitate; Phosphorylation; Repeat; Synaptosome.

19 81 t-SNARE coiled-coil homology 1.

1-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 68; DB 1; Length 206; 100.0%; Pred. No. 0.00068; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP 006186
                                                                                                                                                                                                                                                                                                                                                                         SNAP-25a).
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
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138
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Name=SNAP25;
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85
180
138
187
58
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MOD_RES
VARSPLIC
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HELIX
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STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
X MEDLINE=22354683; PUMPGG=12466851; DOI=10.1038/nature01266;
A MEDLINE=22354683; PUMPGG=12466851; DOI=10.1038/nature01266;
A Nikaido I., Osato N., Saitor R., Suzuki H., Yamanaka I., Kiyosawa H., Nikaido I., Osato N., Baldarelli R., Hall D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., A Blake J.A., Razapin T.A., Pletcher C.F., Forrest A., Frazer K.S., Gassterland T., Gariboldi M., Gissi C., Godzik A., Gaugh J., Aranaind H., Kawasawa Y., Kedzierski R.M., King B.L., Aranain A., Kawasawa Y., Kedzierski R.M., King B.L., Aranain A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
                                                                                                                                                                                                                                                                                                                     P60875; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45; 01-JAN-1990 (Rel. 13, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
13-58P-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated protein) (SUP: Name-Snap25; Synonyms-Snap; Musme-Snap25; Synonyms-Snap; Eukaryors: Whereas Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M., Bloom F.E., Wilson M.C.;
"The identification of a novel synaptosomal-associated protein, SNAP-25, differentially expressed by neuronal subpopulations.";
J. Cell Biol. 109:3039-3052(1989).
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                    Clearage (by BONT/E) (By similarity). Phosphothreonine (By similarity). Phosphoserine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ILS, and ISS;

BUBLINE-218:3810.

Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,

Besson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;

High-throughput sequence identification of gene coding variants

within alcohol-related GTLs.";

Mamm. Genome 12:657-663(2001).
                                                                                                                                                                                                                   ;
0
Pfam; PF00835; SNAP-25; 1.

Pfam; PF05739; SNARE; 1.

SMART; SM0397; t. SNARE; 2.

PROSITE; PS50192; T. SNARE; 2.

Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
                                                                               t-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
Cys-rich.
                                                                                                                                                                                      Length 206;
                                                                                                                                                                                                                0; Indels
                                                                                                                                                             FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                       ; Score 68; DB 1; L; Pred. No. 0.00068; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
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                                                                                                                                                             206 AA; 23315 MW;
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100.0%;
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                                                                                                                                                                                                                                          2 TRIDEANQRATKML 15
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Best Local Similarity lov..
Lag 14; Conservative
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                                                                   Synaptosome.
DOMAIN
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SEQUENCE
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NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).

STRAIN-C57BL/6; TISSUB-EY9;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Moore T., Max S.L., Mand J., Haith N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Mand J., Haith N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wokernan R.J., Makernan R.D., Mullahy S.J.,

Rapak S.A., McEwan P.-G., Marcernan R.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schwultz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Marra M.A.,

Butterfield M.B., Johen J.B., Johes M.C.,

Butterfield M.S., Wolley M. Madan M.A.,

Butterfield M.S., Wolley M. Mara M.A.,

Butterfield M.S., Wolley M. Madan M.A.,

Butterfield M.S., Wolley M. M. Mara M.A.,

Butterfield M.S., Wolley M. M. M. M. Mara M.A.,

Butterfield M.S., Wolley M. M. Mara M.A.,

Butterfield M.S., Wolley M. M. M. M. Mara M.A.,

Butterfield M.S., Wolley M. M. Mara M.A.,

Butterfield M. Mara M.A.,

Butterfield M. M.
Ravai T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Reed D.J., Reid J.C., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Werardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wang Y., Wang I., Yang I., Yang I., Yan Z., Zavolan M., Zhu Y., Zanmer A., Carninol P., Hayatsu N., Aliraki T., Waki K., Kawai J., Aizawa R., Sakaume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa T., Pukuda S., Airaka A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Yanisaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yashishi X., Yashinow W., Waterston R., Lander E.S., Rogers J., Manalysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION SITES THR-138 AND SER-187.

MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3; Hepp R., Cabaniola J.P., Roche P.A.;

Hepp R., Cabaniola J.P., Roche P.A.;

"Differential phosphorylation of SNAP-25 in vivo by protein kinase C. and protein kinase A.";

"In the state of the state of the molecular regulation of resolution of synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.

"In the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.

"STRIAL PART Of the SNARE core complex containing SNAP25, VAMP2 and STRIA. This complex binds CPLX1. Interacts with TRIM9, RIMS1, STRIA and VAMP8 (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10195194; DOI=10.1038/5673;
Ilardi J.M., Mochida S., Sheng Z.-H.;
"Snapin: a SNARE-associated protein implicated in synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Neurosci. 2:119-124(1999).
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IsoId=P60879-2, P13795-2;
Sequence=VSP_010019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P60879-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences."
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CC -1. PFW, Palmikovijaced (By similarity).

CC -1. SIMILARITY: Delongs to the SNRP-25 family.

CC -1. SIMILARITY: Contains 2 t-SNARE colled-coll homology domains.

CC -1. SIMILARITY: Contains 2 t-SNARE colled-coll homology domains.

CC -1. SIMILARITY: Contains 2 t-SNARE colled-coll homology domains.

This Swies-Prot entry is copyright It is produced through a collaboration to the between the Spiels Institute Fel Bioliformatics and the BMB. Outtetation - the Swies Fort entry is copyright It is produced through a collaboration cue as long as its content is in no way modified and this statement is not the BMB. NZ2013, AAM6174111 - mRNA.

DR SWEL, MANSON AAM6174111 - mRNA.

DR SWEL, ARM3316, AAA190790.11 - mRNA.

DR SWEL, BOONO AND AAH1829.1 - mRNA.

DR CO, GO:000149; FISHARE BININGS.

DR CO, GO:000149
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Search completed: April 3, 2006, 15:46:25 Job time: 82.4954 Becs

190 TRIDEANORATION 203

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 3, 2006, 15:30:10 ; Search time 8.66055 Seconds Run on:

(without alignments)
177.756 Million cell updates/sec

US-09-942-098-91 68 Title: Perfect score:

1 XTRIDEANQRATKMLX 16 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result	0100	Query	Query March Length	ä	CI.	Description
	21000	100		1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
-	69	100.0	203	7	150481	
7	68	100.0	204	8	I50480	synapse protein SN
m	68	100.0	206	~	A37861	synaptosomal-assoc
4	68	100.0	206	~	153735	nerve terminal pro
Ŋ	68	100.0	206	7	167823	nerve terminal pro
ø	68	100.0	206	~	A33623	synaptosomal-assoc
7	54	79.4	210	~	150552	synapse protein -
8	42	61.8	83	7	A33854	outer membrane lip
6	41	60.3	2288	~	T29999	
10	40	58.8		~	T34187	hypothetical prote
11	38	55.9		~	G95369	SyrB2 transcriptio
12	38	55.9		N	JC5297	vesicle-membrane f
13	38	55.9		~	D72668	hypothetical prote
14	38	55.9		7	JC5512	SNARE protein 23 -
15	38	55.9		7	JC5296	vesicle-membrane f
16	38	55.9	317	~	A72295	conserved hypothet
17	38	55.9		~	S64386	pre-mRNA splicing
18	38	55.9	_	~	S76238	hypothetical prote
19	37	54.4		٦	RRNZ	phosphoprotein P -
20	37	54.4	241	Н	RRNZPP	phosphoprotein P -
21	37	54.4		7	859660	
22	37	54.4	9	~	S55024	nebulin, skeletal
23	36	52.9		•	C84375	
24	36	52.9		~	T32127	hypothetical prote
52	36	52.9			E81436	č
56	36	52.9	642	7	G90551	
27	36	52.9	99	~	F98020	hypothetical prote
28	36	52.9	680	7	H70347	bra
29	36	52.9	989	Н	E71106	probable DNA topoi

hypothetical prote DNA-directed RNA p hypothetical prote ADP-ribosylation f ADP-ribosylation f probable ATP-bindi protein F16A14.10 hypothetical prote	hypothetical prote exodeoxyribonuclea conserved hypothet
T33167 A29959 D84748 A45422 D83271 T18167 T18167 T05428 B70435 A702473	D84888 G69960 F83519
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ALIGNMENTS

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synapse protein SNAP-25 - goldfish (c)species: Carassius auratus (goldfish) (c)species: Carassius auratus (goldfish) (c)species: Carassius auratus (goldfish) (c)species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 (c)accession: 150481 (c) tarbiammar, D. (c)accession: 150481 (c) tarbiammar, D. (d) tarbiammar, D. (e) tarbiammar, D. (e) tarbiammar, D. (e) tarbiamser: A49632; MUID:94068448; PMID:8248151 (e) tarbiamber: A49632; MUID:94068448; PMID:8248151 (e) tarbiaminary; translated from GB/EMBL/DDBJ (e) tarbiaminary; translated from GB/EMBL/DBJ (e) tarbiaminary; tran
RESULT 1
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Gaps ö Length 203; 0; Indels Query Match
100.0%; Score 68; DB 2; I
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 14; Conservative 0; Mismatches 0;

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187 TRIDEANQRATKML 200 2 TRIDEANORATION 15

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Cyange protein SNAP-25 - goldfish (Syangse protein SNAP-25 - goldfish) (Species: Garassius auratus (goldfish) (Spate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 (Spacession: ISO480 Fords (Spates) (Spates

A;Residues: 1-204 <RIS> A;Cross-references: UNIPROT: P36977; UNIPARC: UPI0000135B02; GB:L22973; NID:g349426; PIDN: P C;Genetics: A;Gene: SNAP-25

Gaps ö Length 204; 100.0%; Score 68; DB 2; Length 20 100.0%; Pred. No. 5.1e-05; iive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 14; Conservative

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188 TRIDEANORATKML 201 2 TRIDEANORATKML 15 g Š

RESULT 3

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Gynapse protein - marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150552
B;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.J.
J; Biol. Chem. 268, 24408-24414, 1993
A;Ritle: Bvolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shc
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Reference number: A49513; MUID:94043281; PMID:826991
A;Reference mumber: A49513; MUID:94043281; PMID:826991
A;Reference mumber: A49513; MUID:94043281; PMID:826991
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A;Residues: 1-210 <RIS
A;Residues: 1-210 <RIS
A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFE; GB:L22020; NID:9431296; PIDN:F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gynaptosomal-associated 25K protein - mouse
Gynaptosomal-associated (house mouse)
Gynapte: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
Gynapte: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
Gynapter, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; V
J. Call Biol. 109, 3039-3052, 1980
A; Fitle: The identification of a novel synaptosomal-associated protein, SNAP-25, differer
A; Reference number: A33623; MUID:90078337; PMID:2592413
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 27-Feb-1990 #sequence revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33854; S04834; A4834; A83288
R;Duchene, M.; Barron, C.; Schweizer, A.; von Specht, B.U.; Domdey, H.
J. Baterioll. 171, 4130-4137, 1989
A;Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, sec
A;Reference number: A33854; MUID:89327122; PMID:2502533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI000001103; GB:M22012; GB:X51673; NID:9200
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                                                                                                          Length 206;
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100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                   100.0%; Score 68; DB 2; 100.0%; Pred. No. 5.2e-05; iive 0; Mismatches 0;
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Pred. No. 0.02;
1; Mismatches
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2
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Local Similarity 84.6%;
es 11; Conservative
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198 RIDEANKHATKML 210
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Best Local Similarity 100.
Matches 14; Conservative
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R;Bark, I C.; Wilson, M.C.
Rene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein A;Reference number: 153735; MUID:94156217; PMID:8112622
A;Accession: 167823
                                                                                                                                                                                                                                                                              Ricatsicas, S.; Larhammar, D.; Blomgvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C. Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid A;Reference number: A37861; MUID:91126080; PMID:1992470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: 153735; MUID:94156217; PMID:8112622
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C;Genetics:
A;Gene: GDB:SNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-206 <CAT>
A,Cross-references: UNIPROT:P60878; UNIPARC:UPI000001103; GB:M57957; NID:g212673; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                          aynaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
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Length 206;

Indels

'Match 100.0%; Score 68; DB 2; L Local Similarity 100.0%; Pred. No. 5.2e-05; Les 14; Conservative 0; Mismatches 0;

Query Match

Best Loc Matches

A;Accession: A37861

Accession: 153735

A; Accession: I53735

Length 206;

Score 68; DB 2; I Pred. No. 5.2e-05; 0; Mismatches 0;

Query Match 100.0%; Best Local Similarity 100.0%; Matches 14; Conservative 0

TRIDEANORATKML 203

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nerve terminal protein - human

A, Cross-references: GDB:355671; OMIM:600322 A, Map position: 20p11.2-20p11.2

A; Gene: GDB: SNAP

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-206 <RES>

Indels

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A;Cross-references: UNIPROT: Q9GYQ4; UNIPARC: UPI000017CE0F; EMBL: U42436; PIDN: AAA83492.1;
                                                                                                                                                                                                                                        hypothetical protein C49H3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 12-Jul-2004
C;Accession: T34187
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A; Description: The sequence of C. elegans cosmid C49H3.
A; Reference number: Z21485
                           4.
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53.8%; Pred. No. 13;
ive 3; Mismatches
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A;Molecule type: DNA
A;Residues: 1-540 <WUX>
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Pred. No. 21;
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4; Mismatches
Pred. No. 63;
2; Mismatches
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58.3%;
     57.1%;
                                                                                                               627 TRIDELNRRVENLL 640
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                                                                         2 TRIDEANORATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: CESP:C49H3.1
A;Introns: 247/2; 319/2; 393/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RIDEANQRATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::|||||| ::|
277 LEEANORADRLL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
     Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 IDEANQRATKML 15
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T34187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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K.; Lim,
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-83 <COR>
A; Residues: 1-83 <COR>
A; Residues: 1-83 <COR>
A; Cross-references: UNIPARC; UPI000002C273; EMBL: X13748; NID: 945344; PIDN: CAA32013.1; PID
A; Cross-references: UNIPARC; UPI0000002C273; EMBL: X13748; NID: 945344; PIDN: CAA32013.1; PID
A; Note: the authors translated the codon GAA for residue 78 as Gly
R; Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R.
A; Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R.
A; Title: Specificity of the Pseudomonas aeruginosa PAO1 lipoprotein I gene as a DNA prob
A; Reference number: A44834; MUID: 92268853; PMID: 1588307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Stauus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2288 <LAT>
A;Residues: 1-2288 <LAT>
A;Cross-references: UNIPROT: Q23081; UNIPARC: UPI000017BCE7; EMBL: U64862; PIDN: AAB52624.1;
A;Experimental source: strain Bristol N2; clone ZC8
                                                                      A,Cross-references: UNIPROT:P11221, UNIPARC:UP1000002C273; GB:M25761; NID:G151334; PIDN: R;Cornells, P.; Boula, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube Mol. Microbiol. 3, 421-428, 1981
A;Title: Cloning and analysis of the gene for the major outer membrane lipoprotein from A;Reference number: S04834; MUID:89313294; PMID:2473376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
Andlecule type: DNA
A;Residues: 1-83 <SAI>
A;Cross-references: UNIPARC:UPI000002C273; GB:X58714; GB:S36066; NID:g433509; PIDN:CAA41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000002C273; GB:AE004712; GB:AE004091; NID:g9948940; PIDN:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: PAO1
A;Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIP:103667)
A;Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIP:103667)
A;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29999
R;Latrellle, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1986
A;Reference number: Z20719
A;Reference number: Z20719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 83;
Pred. No. 1.2;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: oprI; PA2853
C;Keyworde: lipid binding; lipoprotein; membrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-83/Product: lipoprotein I #status predicted <MAI>
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nes 8; Conservative
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DEANERALRML
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A;Molecule type: DNA
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Query Match

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C;Accession: JC5296
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 ir A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Reference number: JC5296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                           ||| || || |:
196 RIDIANTRAKKLI 208
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: O2-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession. JG5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Oka Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Muncl8c.
A;Reference number: JG5512; MUID:97312558; PMID:9168999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kana, H.; Takamiya, M.; Yamazaki, J.; Kana, K.; Saali, 1999 & S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kana, K.; Kamazaki, J.; Kana, K.; Kana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:000161, UNIPARC:UP100002B3DC, GB:Y09568; NID:g1924943, PIDN
A,Experimental source: neutrophils
C,Comment: This protein is involved in regulating exocytosis in human neutrophils, a cer
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A;Residues: 1-210 <ARA>
A;Cross-references: UNIPROT:O09044; UNIPARC:UPI0000022B5C; DDBJ:AB000822; NID:g2189950;
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A;Experimental source: strain Kl
                                                                                                                                                                                                                                                 C; Accession: ÚC5297
R; Mollindo, F; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A; Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23
A; Reference number: ÚC5296; MUID:97224437; PMID:9070898
A; Status: nucleic acid sequence not shown; translation not shown
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72668
                                                                                     vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
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Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 3; Indels
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C,Superfamily: Aeropyrum pernix hypothetical protein APE0770
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A; Residues: 1-158 <MOL>
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A;Molecule type: DNA
A;Residues: 1-176 <KAW>
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Gene: APE0770
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RESULT 12
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C, Comment: This protein is involved in the insulin-induced translocation of vesicles cont
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                                                                          Gaps
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                                       Length 210;
                                   Score 38; DB 2;
Pred. No. 18;
2; Mismatches
                                       Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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3 RIDEANORATKML 15

vesicle-membrane fusion protein SNAP-23A - human

A;Molecule type: mRNA A;Residues: 1-211 «MOL> A;Cross-references: UNIPROT:CO0161; UNIPARC:UPI0000000A2C; GB:Y09567; NID:G1924941; PIDN: C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cent A;Status: nucleic acid sequence not shown; translation not shown

ö Gaps ö Query Match 55.9%; Score 38; DB 2; Length 211; Best Local Similarity 61.5%; Pred. No. 18; Matches 8; Conservative 2; Mismatches 3; Indels

Search completed: April 3, 2006, 15:31:24 Job time: 9.66055 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

April 3, 2006, 15:27:08 ; Search time 82.055 Seconds (without alignments) 85.675 Million cell updates/sec Run on:

US-09-942-098-91 68 Title: Perfect score:

1 XTRIDEANQRATKMLX 16 Sequence: 2443163 seqs, 439378781 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 21:* •• Database

geneseqp20018:* geneseqp20028:* geneseqp20038:* geneseqp2003bs:* geneseqp20058:* geneseqp1990s:* geneseqp2000s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description			FRET	FRET E	Aay44057 Human SNA	Aay44021 Amino aci		Human	_		_	Human	Aae36677 Human SNA	Abw01733 Human SNA	Adm97048 Botulinum	Human	Aab15586 Human SNA				Abw01793 FRET subs		FRET	Adp13171 SNAP 25 p
GI GI	AAE36736	AAE36739	ABW01795	ABW01792	AAY44057	AAY44021	ABG69065	AAE36675	ABW01731	ADM97046	ADM97062	AEA14920	AAE36677	ABW01733	ADM97048	AEA14922	AAB15586	AAE36730	AAE36740	AAE36737	ABW01793	ABW01796	ABW01786	ADP13171
DB	٥	9	7	7	N	N	ស	9	7	80	Φ	6	φ	~	æ	0	4	9	9	9	7	7	7	œ
Query Match Length DB	16	16	16	16	17	17	17	17	17	17	17	17	18	18	18	18	13	19	19	19	19	19	19	19
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	69	89	89	68	89	68	68	68	68	69		89	89		89	89	9	89				89	89	68
	-	7	m	4	ď	v	7	60	σ	10	11	12		14	15	16	17	18	19	20	21	22	23	24

AAW30100 Aaw30100 Neurotran ABW01798 FRET subs AAE36734 Fret subs AAEW01790 FRET subs AAEW01790 FRET subs AAEW01794 FRET subs AAEM36733 AAE36738 Fret subs AAEM36733 AAE36735 Fret subs AAEM36735 Fret subs AAEM36735 AAW30099 FRET subs AAEM3682 AAEM3682 AAEM3682 AAEM3682 AAEM3682 AAEM3682 AAEM3682 AAEM3682 AAEM3682 AAEM3683 AAEM3682 AAEM3683 AAEM37083 AAE	ALIGNMENTS 6 AA.			in t	otease activity; botulinum toxin; BoNT; TeNT; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;		Location/Qualifiers 1 1 1 1 1 1 1 1 1 1 1 1 1	"Tetramethylrhodamine-modified Lysine; C-terminal This residue is given as Xaa in the sequence shown ID NO: 91 in the sequence listing of the cation"						B, Aoki KR;		utrate useful for assaying protease activity of donor fluorophore, acceptor and a clostridial that includes a cleavage site.	English.
001100mm449mmmmmmmmmmmmmmmmmmmmmmmmmmmmm	peptide;		entry)	#7 used	protease ; synapto		tion/Qua e= "Fluo n as Xaa sequence				1027145	94202		-Salas		subs rises ence	168pp;
ลัสลิลลิลิลิลิลิลิลิลิลิลิลิลิลิลิลิลิลิ				peptide	Ä		Location 1 / note= given the se	16 /note= amide; as SEQ specif			002WO-US02	2001US-00	INC.	Fernandez	/28.	a)	115; 1
000000000000000000000000000000000000000	standard;		(first	ø	toxin; E n; VAMP;		O)	Φ	-A2.		7		ALLERGAN	Fer	/8610	num serotype num toxins, c recognition s	age
	stai		003	substrat	ium toxi	fied	-81	-sit	0948	-2003.	002;	2001;	ALLE	LE,	3-29	m se m to cogn	1; P
\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	T 1 736 AAE36736	AAE36736	07-AUG-2	ret	Clostridium to tetanus toxin; cosmetic.	Unidentif	Key Modified	Modified	WO20030209	13-MAR-2	22-AUG-2	28-AUG-2	(ALLR)	Steward	WPI; 2003	Botulinum botulinum toxin rec	Example
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	36 36			DE			AHTTTT							_	_		*

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            invention further relates to be united programs countries which comprise a donor fluorophore, an acceptor having an absorbance appetrrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BoNT/B recognition spectrum of the donor fluorophore and a BoNT A or BoNT/B recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the procease activity of any clostridial toxin including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast samples consist of the supersessed foods, beverages, animal feed, soil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum serotype A/E substrate useful for assaying protease activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "DABCYL-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 94 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "EDANS-modified Glutamate; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 94 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                               purification
                                                                                                                                                                                                                                                 samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 68; DB 6; Length 16; 100.0%; Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fret substrate peptide #10 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE36739 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2002; 2002WO-US027145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001US-00942024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TRIDEANQRATKML 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-290198/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003020948-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE36739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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inte present interaction to the control substrates to invention further relates to botulinum serotype A/B (BONT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (Synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay tormulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
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botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                 the present invention relates to novel clostridium toxin substrates. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRET substrate #8 to analyse proteolytic activity of botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "EDANS labelled glutamate; C-terminal amide"
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 68; DB 6; Length 16; 100.0%; Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "DABCYL labelled lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steward LE, Fernandez-Salas E, Aoki KR;
                                                             Example 1; Page 115; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABW01795 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2001; 2001US-00942098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8-AUG-2001; 2001US-00942098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TRIDEANORATKML 15
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Best Local Similarity 100.0
Each of 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2004 (first entry)
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(FERN) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-829791/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABW01795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
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proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention

Sequence 16 AA;

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clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 29; Opp; English
                                                                                                                                           Unidentified
                                                                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                     31-JUL-2003
                                                                                                                                                                                                ABW01792;
                                                                                                         Query Match
                                                                                                                Best Loca
Matches
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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                  The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 68; DB 7; I 100.0%; Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                   Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TRIDEANORATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                   Example 1; Page 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16 AA;
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Determining clostridial toxin protease activity, by treating sample with
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amide"
                                                                                                                                                                                         Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                                                                          FRET substrate #5 to analyse proteolytic activity of botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                     'note= "Fluoresceinated lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aoki KR
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
ABW01792 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001US-00942098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (STEW/) STEWARD L E.
(FERN/) FERNANDEZ-SALAS E.
                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS2003143651-A1
                                                                                                                                                                                                                                                                                                                            Key
Modified-site
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The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum coxin, by determining the proteolytic activity of botulinum coxin A has neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample conteaining the botulinum coxin A so that buman SNAP25 to a sample conteaining the botulinum coxin A so that can each time point by combining with a label capable of detecting free at each time point by combining with a label capable of detecting free amount of botulinum toxin A present in the sample is determined by comparing measured amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of
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                                                                                                                                                                                                                                                                                                                           // quantitation, type A botulinum neurotoxin, proteolysis, detection, human, synaptosomal protein, SNAP25;
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                                               Gaps
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           100.0%; Score 68; DB 7; Length 16; 100.0%; Pred. No. 3.1e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 68; DB 2; L ilarity 100.0%; Pred. No. 3.4e-05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              Human SNAP25 (amino acids 187-203) analogue #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quantitation of type A botulinum toxin.
                                                                                                                                                                                             AAY44057 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Col 9; 28pp; English.
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Query Match
Best Local Similarity
Local Similarity
Set Local Similarity
The Conservative
                                                                                 2 TRIDEANQRATKML 15
                                                                                                    2 TRIDEANORATION 15
                                                                                                                                                                                                                                                               18-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  hydrolysis; amino group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSA ) US SEC OF ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type A botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                  Enzymatic assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                   luorescamine;
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Best Local Simil
Matches 14; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-0CT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                US5965699-A
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                 AAY44057;
                                                                                                                                                                  RESULT 5
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Indels

2 TRIDEANORATKWL 15

4 TRIDEANQRATKML 17

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The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum acurotoxin type A using fluorescanine detection. The method comprises adding an analogue (e.g. AAV44022-Y44076) of this peptide (which represents amino acids 187-203 of the human synaptosomal protein SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is intirated, then stopping hydrolysis of the peptide is intirated, then sucuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of
                                                                                                                                                          Enzymatic assay, quantitation; type A botulinum neurotoxin; proteolysis;
fluorescamine; detection; human; synaptosomal protein; SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 3.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quantitation of type A botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide C-terminal fragment.
                                                                                                                          Amino acids 187-203 of human SNAP25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69065 standard; peptide; 17 AA.
                              AAY44021 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 4; 28pp; English.
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                                                                                            18-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt JJ;
                                                                                                                                                                                          hydrolysis; amino group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type A botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                       (USSA ) US SEC OF ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-579939/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 AA;
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                        06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                        06-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Bostian KA,
                                                                                                                                                                                                                                                                                        12-OCT-1999
                                                              AAY44021;
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Matches
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RESULT 6
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                AAY4402
                                             XXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, clostridium toxin, protease activity, botulinum toxin, BoNT; TeNT,
tetanus toxin, VAMP, synaptobrevin, SNAP-25, syntaxin, pharmaceutical,
Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain; spasticity, ocular motility; facial dyskinesia; stiff-person syndrome; bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human; cosmetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant; lower motor neuron hyperactivity; autonomic nerve function; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule encoding botulinum neurotoxin light chain serotype A, useful for producing the neurotoxin for vaccination against botulism, comprises sequence expressible in host other than Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                              (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
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                                                                                                     Immunostimulant; antibacterial
                                                                                                                                                                                                                                                                                             06-NOV-2000; 2000US-0246774P.
20-JUL-2001; 2001US-00910186.
09-AUG-2001; 2001US-0311966P.
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Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SNAP-25 peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                    Smith LA, Jensen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-575192/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 AA;
                                                                                                                                                                                 WO200236758-A2.
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the invention
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                                                                                                                                             Homo sapiens.
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Homo sapiens

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28-AUG-2001; 2001US-00942098.

WO2003020948-A2

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BoNT/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance apectrum overlapping the emission spectrum of the donor fluorophore and a BONT/B recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast toxins water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification or process. The present sequence is human or sunance to the sunance or sunance to sunance to sunance and sunance to sunance the sunance to sunance the sunance to sunance sunance sunance sunanc
                                                                                                                                                                                                                                                                                                                                         Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 68; DB 6; Length 17; 100.0%; Pred. No. 3.4e-05; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                               Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNAP-25 peptide used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 40, 168pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABW01731 standard; peptide; 17 AA
                                                                                                                                                                                                                                               Fernandez-Salas E,
                                                                                            22-AUG-2002; 2002WO-US027145
                                                                                                                                              28-AUG-2001; 2001US-00942024
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                              WPI; 2003-290198/28.
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                                                                                                                                                                                                                                                  Steward LE,
                                            13-MAR-2003
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                                                                                                                                            Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening
                                                                                                                                                                                                                                        The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food
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                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 68; DB 7; Length 17; 100.0%; Pred. No. 3.4e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 52; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aoki KR;
                                                                                     Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM97046 standard; peptide; 17 AA.
                                                                                                                                                                                                              Disclosure; Page 10; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandez-Salas E, Steward LE,
                                                                                       Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2003; 2003WO-US028092.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TRIDEANQRATKML 15
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                           STEW/) STEWARD L E. FERNANDEZ-SALAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-340456/31.
                                                                                                                    WPI; 2003-829791/77.
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                                                          AOKI/) AOKI K R.
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                                                                                                                                                                                                                                                                                                                                         Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Gaps

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28-AUG-2001; 2001US-00942098

31-JUL-2003

transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the contacted cell is indicative of clostridial toxin activity. (M1) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (M1) is an automated high-throughput assay. (M1) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and procease activity. In the method M1, the clostridial toxin substrate is a botulinum toxin substrate comprising a BoNT/B, BONT/C, BONT coxin substrate

Sequence 17 AA;

Gaps ö Score 68; DB 8; Length 17; Pred. No. 3.4e-05; 0; Mismatches 0; Indels Query Match 100.0%; Best Local Similarity 100.0%; Matches 14; Conservative C 2 TRIDEANORATKML 15 ઠે

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4 TRIDEANQRATKML 17

Botulinum toxin substrate recognition sequence #47. ADM97062 standard; peptide; 17 AA. (first entry) 01-JUL-2004 ADM97062; RESULT 11 ADM97062

IID ADM9

IID ADM9

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ADM9

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ADM9

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ADM9

B Botuu

ADM9

B Botuu

ADM9

clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.

Synthetic

WO2004029576-A2

08-APR-2004

04-SEP-2003; 2003WO-US028092.

27-SEP-2002; 2002US-00261161

(ALLR) ALLERGAN INC

Aoki KR; Steward LE, Fernandez-Salas E,

WPI; 2004-340456/31.

Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.

Disclosure; SEQ ID NO 68; 188pp; English.

The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (P), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the

ö contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (MI) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (MI) is an automated high-throughput assay. (MI) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and protease activity. In the method MI, the clostridial toxin substrate is a botulinum toxin substrate selected from a BONT/A, BONT/B, BONT/C, BONT/F, a recognition sequence for a botulinum toxin used as the clostridial Determining clostridial toxin protease activity, by treating sample with tagged toxin substrate comprising fluorescent protein, first and second partner of affinity couple and assaying fluorescent cleavage product in Gaps Human SNAP-25 substrate BoNT/A recognition sequence, SEQ ID NO: 30. ; 100.0%; Score 68; DB 8; Length 17; 100.0%; Pred. No. 3.4e-05; ive 0; Mismatches 0; Indels Neurotoxin; fluorescence; SNAP-25; botulinum toxin. AEA14920 standard; peptide; 17 AA. Steward LE, Gilmore MA, Aoki KR; 13-AUG-2004; 2004US-00917844. 28-AUG-2001; 2001US-00942098. (ALLR) ALLERGAN SALES INC. 2 TRIDEANORATKWL 15 4 TRIDEANORATKML 17 14-JUL-2005 (first entry) 14; Conservative WPI; 2005-365632/37. Query Match Best Local Similarity toxin substrate US2005100973-A1 Sequence 17 AA; Homo sapiens. 12-MAY-2005. AEA14920; reated Matches RESULT 12 **AEA14920** 888888888888888888888888 셤

The present invention relates to a method for determining protease activity of clostridial neurotoxins such as botulinum neurotoxin (BONT) and tetamus neurotoxin (TeNT). The method involves treating with a sample, in solution phase under conditions suitable for clostridial toxin protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, souples and clostridial toxin recognition sequence comprising fluorescent protein, first partner of affinity couple and clostridial toxin recognition sequence comprising cleavage site; contacting treated sample with second partner of affinity couple; and assaping present elevance clostridial sequence is the human SNAP-25 substrate BONT/A (botulinum neurotoxin serotype A) recognition sequence. Disclosure; SEQ ID NO 30; 97pp; English.

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Mismatches

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RESULT 13 AAE36677

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                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inte present interaction to control to control to comprise a donor fluorophore, an acceptor having an absorbance which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the processe activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast toxins (TeNT) in a sample, tissue samples and beverage or food samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification or control or having one or more symptoms of a not location and cosmetics. The present sequence is human control or human or man and purification control.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human, clostridium toxin, protease activity, botulinum toxin, BoNT, TeNT,
tetanus toxin, VAMP, synaptobrevin, SNAP-25, syntaxin, pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to novel clostridium toxin substrates. The
                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 6; Length 18; Pred. No. 3.6e-05;
                                                        Length 17;
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                                                        ; Score 68; DB 9; I
; Pred. No. 3.4e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 40-41; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNAP-25 peptide used in the invention
                                                                                                                                                                                                                                                                     AAE36677 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steward LE, Fernandez-Salas E,
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                                                          Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2001; 2001US-00942024.
                                                                                                                                  2 TRIDEANQRATKML 15
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                                                                                                                                                                                                                                                                                                                                                                                      Human SNAP-25 peptide #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-290198/28.
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                         Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
                                                                                                                                                                                                                                                                                                                                                                                      Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
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                                                                                                                                                                                                                                                                                                                                     Human SNAP-25 BoNT/A recognition peptide #6.
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                                                                                                                                                                                ABW01733 standard; peptide; 18 AA.
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FERNANDEZ-SALAS
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The invention relates to a method of determining (MI) clostridial toxin activity, comprising contacting cell with sample comprising clostridial activity, comprising contacting cell with sample comprising clostridial coxin method for fluorophore (F), acceptor (A) with an absorbance appectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening clostridial toxin recognition sequence with cleavage site intervening transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (MI) is useful control cell is indicative of clostridial toxin activity, where the sample is a crude cell repart of the contacted cell as compared clostridial toxin, formulated clostridial toxin, formulated clostridial toxin, product, BOTOX or food. (MI) is an automated high-throughput assay. (MI) reduces the need for animal toxicity studies and serves to analyze contacted from a BOMT/A, BOMT/B, BOMT/CI, CANCER CONTENTIBLE CONTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 54; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                Aoki KR;
                                                                                                                                                                                                                                                                                                                                                Steward LE,
                                                                                                                                                                      04-SEP-2003; 2003WO-US028092.
                                                                                                                                                                                                                                27-SEP-2002; 2002US-00261161
                                                                                                                                                                                                                                                                                          (ALLR ) ALLERGAN INC.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-340456/31
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Homo sapiens.
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Query Match 100.0%; Score 68; DB 8; Length 18; Best Local Similarity 100.0%; Pred. No. 3.6e-05; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: April 3, 2006, 15:36:57 Job time : 83.2217 secs

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Sequence 40, 1
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346B 0097- 0071- 0071- 0071- 0071- 0071- 0071- 0071- 0071- 0071-	ENTS bellic 71	ore 84; D ed. No. 7. Mismatches 1 red Substraing Clostrii
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	ALIGNME ESULT 1 S-10-947-071-36 Sequence 36, Application US/10947071 Publication No. US20060063221A1 APPLICANT: Williams, Dudley J. APPLICANT: Gilmore, Marcella APPLICANT: Gilmore, Marcella APPLICANT: Gilmore, Marcella APPLICANT: Graward, Lance APPLICANT: Aoki, Kei Roger APPLICANT: Aoki, Kei Roger APPLICANT: Aoki, Kei Roger TITLE OF INVENTION: Lanchanide-Based Sub TITLE OF INVENTION: 2004-09-21 NUMBER OF SEQ ID NOS: 101 SEQ ID NO 36 LENGTH: 33 TYPE: REFERENCE: GENTION WINDOWS VETSION 4. SEQ ID NO 36 LENGTH: 33 TYPE: PRT ORGANISM: MNS musculus 15-10-947-071-36	
00000000000000000000000000000000000000	RESULT US-10- US-10- S-10- S-10- S-10- S-10- S-10- RESULT	Ouery hat cheek
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Publication No. US20060063222A1
GENERAL INFORMATION:
APPLICANT: Verhagen, Marc
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                                                                      2 TRIDEANQRATKMLGSG 18
                                                                                                                                      17 TRIDEANORATKMLGSG 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 17; Conservative
   17; Conservative
                                                                                                                                                                                                                                                                            US-10-948-097-40
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US-11-195-098-11
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LENGIH: 33
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US-10-947-071-41

Sequence 41, Application US/10947071

Sequence 41, Application US/10947071

Publication No. US20060063221A1

GENERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Lance
APPLICANT: Verha
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APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Glimore, Marcella
APPLICANT: Greward, Lance
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 33
| TYPE: PRT
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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Pred. No. 7.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 100.0%; Score 84; DB 6; Length 33 Local Similarity 100.0%; Pred. No. 7.7e-09; les 17; Conservative 0; Mismatches 0; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40 LENGTH: 33
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; Sequence 36, Application US/10948097
; Publication No. US20060053222A1
; GENERAL INFORMATION:
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                                                                                                          TYPE: PRT

ORGANISM: Carassius auratus
US-10-947-071-40
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US-10-947-071-41
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US-10-948-097-36
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Best Local Similarity
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Sequence 41, Application US/10948097

Publication No. US20060061222A1

GENERAL INFORMATION:

APPLICANT: Verhagen, Marc

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

TITLE OF INVENTION: Plucrescence Polarization Assays For

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-040

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Williagen, Dudley J.
APPLICANT: Williagen, Dudley J.
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Pluorescence Polarization Assays For
TITLE OF INVENTION: Determining Clostridial Toxin Activity
TITLE OF INVENTION: Determining Clostridial Toxin Activity
TITLE OF INVENTION: Determining Clostridial Toxin Activity
CURRENT APPLICATION NUMBER: US/10/948,097
CURRENT FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 33
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100.0%; Score 84; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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genemon No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Gilmore, Marcella

APPLICANT: Steward, Lance

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Lanthanide-Based Substrates and Methods

TITLE OF INVENTION: For Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-043

CURRENT FILING DATE: 2004-09-21

CURRENT FILING DATE: 2004-09-21

NUMBER OF SEQ ID NOS: 101

SOFTHARE: FASTESQ for Windows Version 4.0
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                                                                                                   APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marc
APPLICANT: Gilmore, Marcella
APPLICANT: Gilmore, Marcella
APPLICANT: Aci, Kei Roger
TITIE OF INVENTION: Plucescence Polarization Assays For
TITIE OF INVENTION: Determining Clostridial Toxin Activity
TITIE OF INVENTION: Determining Clostridial Toxin Activity
TITIE OF STORM NUMBER: US/10/948,097
CURRENT PAPLICATION NUMBER: 2004-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 203
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; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc;
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 84; DB 6; Length 20
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 84; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 17; Conservative 0; Mismatches 0;
Sequence 4, Application US/10948097
Publication No. US20060063222A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Carassius auratus
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LENGTH: 206
TYPE: PRT
CRGANISM: Homo sapiens
US-10-947-071-1
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US-10-947-071-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                   APPLICANT: Schmidt, James J.
APPLICANT: Schmidt, James J.
APPLICANT: Schmidt, James J.
APPLICANT: Schmidt, James J.
APPLICANT: Schmidt, Schmidt, James J.
APPLICANT: Schmidt, Schmidt, Schmidt, Schmidt, Schmidt, Stafford, Robert G.
TITLE OF INVENTION: Neurocroxins
TITLE OF INVENTION: Neurocroxins
FILE REFERENCE: 003/224/SAP
CURRENT PILING DATE: 2002-08-02
FRIOR APPLICATION NUMBER: US/10/802,574
FRIOR APPLICATION NUMBER: 09/962,360
FRIOR PELLING DATE: 2000-09-25
FRIOR PELLING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 11
SEQ ID NO 11
LENGTH: 116
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; Sequence 4, Application US/10947071
; Publication No. US20660063221A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Dudley J.
    APPLICANT: Gilmore, Marcella
    APPLICANT: Steward, Lance
    APPLICANT: Verhagen, Marc
    APPLICANT: Ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 84; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; IOCATION: 1; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-11-195-098-11
           Sequence 11, Application US/11195098
Publication No. US20050287622A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 TRIDEANQRATKMLGSG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPB: PRT ORGANISM: Artificial sequence
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US-10-947-071-4
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Length 206;

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Query Match 100.0%; Score 84; DB 6; Length 20 Best Local Similarity 100.0%; Pred. No. 6.4e-08; Matches 17; Conservative 0; Mismatches 0; Indels
     ; ORGANISM: Mus musculus US-10-948-097-2
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US-10-948-097-2
Sequence 2, Application US/10948097
Publication No. US2060063222A1
GENERAL INFORMATION:
APPLICANT: Verhagen, Marc
APPLICANT: Verhagen, Marcella
APPLICANT: Steward, Lance
APPLICANT: Steward, Lance
APPLICANT: APPLICANT: APPLICANT: Steward, Lance
APPLICANT: APPLI
TITLE OF INVENTION: For Determining Clostridial Toxin Activity FILE REFERENCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 2
LENGTH: 206
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; Sequence 1, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
    APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
    APPLICANT: Gilmore, Marcella
    APPLICANT: Golfore, Marcella

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100.0%; Score 84; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-10-947-071-2
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ORGANISM: Homo sapiens
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US-10-948-097-1
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18-11-169-041-225

Sequence 225, Application US/11169041

Publication No. US20060019284A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: DENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF

TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

FILE REPERENCE: 10001 NP

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT APPLICATION NUMBER: 60/584,405

PRIOR APPLICATION NUMBER: 60/584,405

PRIOR PILING DATE: 2004-06-30

NUMBER OF SEQ ID NOS: 527

SOFTWARE: Patentin version 3.2

SEQ ID NO 225

LENGTH: 206
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Sequence 20, Application US/10947071

Publication No. US20060063221A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Verhagen, Marc

APPLICANT: Verhagen, Marc

APPLICANT: Verhagen, Marc

APPLICANT: Proceed Company of the Company of TITLE OF INVENTION: Larchanide-Based Substrates and Methods

TITLE OF INVENTION: Larc
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; CTHER INFORMATION: Plasmid pQBI GFP-SNAP25
US-10-947-071-20
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2 TRIDEANQRATKMLGSG 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT , ORGANISM: Homo sapiens US-11-169-041-225
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Mon Apr 3 16:29:21 2006

Search completed: April 3, 2006, 15:58:09 Job time: 10.1101 secs

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LOCATION: 19
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 84; DB 3; Length 19;
100.0%; Pred. No. 1e-07;
tive 0; Mismatches 0; Indels
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Sequence 92, Application No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Fer Protease Assays For Botulinum
TITLE OF INVENTION: Sarotype A/F Toxins
FILE REFERENCE: P-AR 4803
CURRENT FILING SAROTY NUMBER: US/09/942,024
CURRENT FILING SARE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
LENGTHARE: PastSEQ for Windows Version 4.0
LENGTH: 19
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APPLICANT: Fermandez-Salas, Ester; APPLICANT: APA, Rei Roger; APLICANT: APA, Rei Roger; TITLE OF INVENTION: Fret Protease Assays For Botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa=fluorescein-modified lysine
US-09-942-098-14
US-10-261-161-7
US-10-942-024-14
US-09-942-024-7
US-09-942-024-7
US-09-942-098-12
US-09-942-098-12
US-09-942-098-12
US-10-261-161-4
US-110-261-161-4
US-110-261-161-8
US-10-261-161-109
US-10-261-161-109
US-10-261-161-109
US-10-261-161-109
US-10-273-860-1223
US-10-917-844-12
US-10-917-844-90
US-10-917-844-90
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i OTHER INFORMATION: at the C-terminal
US-09-942-024-92
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ORGANISM: Artificial Sequence
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Sequence 112, App
Sequence 11, Appl
Sequence 11, Appl
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                                                                                                                                                                                                                                                          April 3, 2006, 15:46:49; Search time 81.7523 Seconds (without alignments) 97.107 Million cell updates/sec
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3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                                                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-942-098-93
US-09-942-024-93
US-09-942-024-90
US-09-942-024-90
US-09-942-024-31
US-09-942-024-33
US-09-942-098-33
US-10-261-161-59
US-10-261-161-59
US-10-917-844-33
US-10-917-844-33
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 39. Application US/09942098
Publication No. US2003014361A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Ferrandez-Salas, Ester
APPLICANT: Ferrandez-Salas, Ester
TILLE OF INVENTION: Fret Protease Assays For Clostridial
TILLE OF INVENTION: Toxins
FILE REPRENCE: P-AR 4802
CURRENT APPLICATION UNMER: US/09/942,098
CURRENT PILLING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 93, Application US/09942024 |
| Sequence 93, Application US/09942024 |
| Sequence 93, Application US/09942024 |
| Fublication No. US2003014365041 |
| GENERAL INFORMATION: |
| APPLICANT: Steward, Lance E. |
| APPLICANT: Fernandez-Salas, Ester |
| APPLICANT: Aoki, Kei Roger |
| TITLE OF INVENTION: Fret Protease Assays For Botulinum |
| TITLE OF INVENTION: Serotype A/E Toxins |
| FILE REPERENCE: P-AR 4803 |
| CURRENT APPLICATION NUMBER: US/09/942,024 |
| CURRENT FILING DATE: 2001-08-28 |
| NUMBER OF SEQ ID NOS: 96 |
| SEQ ID NO 93 |
| LENGTH: 22 |
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TOTHER INFORMATION: Xaa=fluorescein-modified lysine NAME/KEY: MOD_RES
LOCATION: 22
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OTHER INFORMATION: SYNTHETIC peptide
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
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OTHER INFORMATION: at the C-terminal
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OTHER INFORMATION: at the C-terminal
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                        JS-09-942-098-95
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NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 19
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
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; Sequence of Application US/09942098
; Publication No. US20030143651A1
; GENERAL INPORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; TITLE OF INVENTION: Toxins
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION UNDBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
LENOTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa-DABCYL modified lysine NAME/KEY: MOD_RES LOCATION: 19 LOCATION: MAME/KEY: AMIDATION
; TITLE OF INVENTION: Serotype A/E Toxins; FILE REFERENCE: P-AR 4803; CURRENT APPLICATION NUMBER: US/09/942,024; CURRENT FILING DATE: 2001-08-28; NUMBER OF SEQ ID NOS: 96; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEX: MOD_RES
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OTHER INFORMATION: at the C-terminal
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 17; Conserv
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ORGANISM: Artificial Sequence
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Matches 17; Conserva
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US-09-942-098-93
Sequence 93. Application US/09942098
Sequence 93. Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Pernandez-Salas, Ester
APPLICANT: Pernandez-Salas, Ester
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Pret Protease
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER: OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 84; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
; Score 84; DB 3; Length 22; ; Pred. No. 1.2e-07; 0; Mismatches 0; Indels
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US-09-942-024-88

Sequence 88, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kel Roger

TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AA 4803

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 88

LENGTH: 23

LENGTH: 23
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OTHER INFORMATION: synthetic peptide
NAMEK TOPORATION: synthetic peptide
LOCATION: 1
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OTHER INFORMATION: at the C-terminal
         100.0%;
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                                                                                                                        5 TRIDEANQRATKMLGSG 21
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         Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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US-09-942-098-88
Sequence 88, Application US/09942098
Sequence 88, Application Wo. US20030143651A1
Sequence 88, Application No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Acei, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Fret Protease
FILE REPERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT PILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)
; LOCATION: (0)
; CTHER INFORMATION: at the C-terminal
US-09-942-024-88
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                                                                                                                                                                                                                                                 Query Match
100.0%; Score 84; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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Publication No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Apki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Service A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1 -- COTHER INFORMATION: Xaa=fluorescein-modified lysine NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 84; DB 3; I
100.0%; Pred. No. 1.3e-07;
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OTHER INFORMATION: synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
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TYPE: PRT
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                                                                                                                                           NAME/KEY: MOD RES
LOCATION: 1
TOTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD RES
LOCATION: 24
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1

OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAMEN MOD RES
LOCATION: 24

OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAMEN KRY: AMIDATION
LOCATION: (0) ...(0)
OTHER INFORMATION: at the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 84; DB 3; Length 24; Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-942-098-90

Sequence 90, Application US/09942098

Publication No. US2000143651A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Pernandez-Salas, Ester
APPLICANT: Pernandez-Salas, Ester
APPLICANT: Pernandez-Salas, Ester
TITLE OF INVENTION: Pret Protease Assays For Clostridial
FILE REPERSENCE: P-AR 4802
FILE REPERSENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 24
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANIEM: Artificial Sequence
PEATURE:
POTHER INFORMATION: synthetic peptide
NAME/KEX: MOD_RES
                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: at the C-terminal US-09-942-024-90
                                                                                                      FEATURE:
OTHER INFORMATION: synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TRIDEANORATKMIGSG 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TRIDEANORATKMLGSG 18
                                                           TYPE: PRT ORGANISM: Artificial Sequence
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les 17; Conservative
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US-09-942-024-33
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                 SEQ ID NO 90
LENGTH: 24
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Matches
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Sequence 33, Application US/09942024 Publication No. US20030143650A1 GENERAL INFORMATION:

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100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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| Sequence 38, Application US/09942024
| Publication No. US20030143650A1
| GENERAL INFORMATION:
| APPLICANT: Steward, Lance E.
| APPLICANT: Steward, Lance E.
| APPLICANT: Fernandez-Salas, Ester
| APPLICANT: AORI, Kel ROGE
| TITLE OF INVENTION: Serotype A/E Toxins
| FILE REPERENCE: PAR 4803
| CURRENT APPLICATION NUMBER: US/09/942,024
| CURRENT FILING DATE: 2001-08-28
| NUMBER OF SEQ ID NOS: 96
| SOFTWARE: PASESEQ for Windows Version 4.0
| SEQ ID NO 38
| LENGTH: 33
APPLICANT: Ferrandez-Salas, Ester
APPLICANT: Ferrandez-Salas, Ester
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ferrandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OP INVENTION: Fret Protease Assays For Botulinum
TITLE OP INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TRIDEANQRATKMLGSG 18
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US-09-942-024-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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Job time : 82.7523 secs
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100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                   ; Score 84; DB 3; Length 33; Pred. No. 2e-07; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      RESULT 14

US-09-32

US-09-42-098-33

§ Sequence 33, Application US/09942098

§ Bublication No. US2000143651A1

§ GENERAL INFORMATION:

§ APPLICANT: Steward, Lance E.

§ APPLICANT: Permandez-Salas, Ester

APPLICANT: Port, Kei Roger

† TITLE OF INVENTION: Pret Protease Assays For Clostridial

† TITLE OF INVENTION: Treat Protease Assays For Clostridial

† TITLE OF INVENTION: Toxins

FILE REFRENCE: P-AR 4802

† CURRENT APPLICATION NUMBER: US/09/942,098

† CURRENT FILING DATE: 2001-08-28

† SOFFWARE: PRESSEQ for Windows Version 4.0

† SEQ ID NO 33

LENGTH: 33
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Sequence 37, Application US/09942098

Sequence 37, Application US/09942098

Publication No. US20030143651A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE RFERENCE: P-AR 4802
CURRENT FPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 37
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                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0.
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; ORGANISM: Carassius auratus
US-09-942-098-37
  ; ORGANISM: Carassius auratus
US-09-942-024-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-09-942-098-33
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Search completed: April 3, 2006, 15:57:06

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Sequence 9, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
APPLICANT: MONTAL NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flah & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
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100.0%; Pred. No. 6.5e-08;
tive 0; Mismatches 0;
US-08-743-894B-42
US-08-743-894B-50
US-08-743-894B-30
US-08-743-894B-24
US-08-743-894B-24
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-34
US-08-743-894B-34
US-08-743-894B-45
US-09-976-535A-2
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1: 4225 Executive Square, Suite 1400
La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Taylor, Stacy L. REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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STRANDEDNESS: not relevant
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Best Local Similarity 100.0
Matches 17, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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STATE: C
COUNTRY:
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            6622222333
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103.582 Million cell updates/sec
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Sequence 10,
Sequence 10,
Sequence 10,
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Sequence 18,
Sequence 1,
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                                                                                                                                                                                April 3, 2006, 15:31:39 ; Search time 15.1651 Seconds
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Sequence 2
Sequence 2
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                                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-015-960-10

US-09-534-572-10

US-09-962-360B-11

US-09-949-016-6311

US-09-949-016-10671

US-09-949-016-10671

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US-09-949-016-10671

US-09-943-894B-1

US-08-743-894B-1

US-08-743-894B-1

US-08-743-894B-3

US-08-743-894B-49

US-08-743-894B-49

US-08-743-894B-49

US-08-743-894B-30

US-08-743-894B-30

US-08-743-894B-30

US-08-743-894B-30

US-08-743-894B-30

US-08-743-894B-30

US-08-743-894B-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                      1 XTRIDEANQRATKMLGSGX 19
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                              US-09-942-098-92
84
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Match Length DB
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100.0
100.0
100.0
92.9
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Gaps

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Length 20; Indels

Score

Result No.

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202-371-2543
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STREET: 11
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US-08-760-001-10
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Patent No. 6169074

GENERAL INFORMATION:
APPLICANT: Monutal, Mauricio
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: DEUROFRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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MEDIUM TYPE: Floppy disk
COMPUTER: He PC compatible
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPOSINE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTONREY/AGENT INFORMATION:
NAME: TAYLOR, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION INFORMATION:
TELEPHANE 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LEMETHE COMPUTER CHARACTER CHARACTER
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Pred. No. 8.7e-08;
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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                                                                                                                                                                          Sequence 8, Application US/08819286
Patent No. 6169074
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STRANDEDNESS: not relevant
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4 TRIDEANQRATKMLGSG 20
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Best Local Similarity 100.0
Matches 17; Conservative
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MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
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STATE:
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COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
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100.0%; Score 84; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0;
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                                                                                                                  Sequence 10, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 156
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: peptide
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Sequence 10, Application US/09534572;
Sequence 10, Application US/09534572;
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Halls, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Oulnn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Weahington
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                         JS-09-534-572-10
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RESULT 6
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Sequence 10, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington
                                                                                                                                                                                    Query Match 100.0%; Score 84; DB 1; Length 70; Best Local Similarity 100.0%; Pred. No. 2.7e-07; Matches 17; Conservative 0; Mismatches
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100.0%; Score 84; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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ZIP: 20005-3934
COMPUTER RADABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.013
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                       2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                   54 TRIDEANQRATKMLGSG 70
    information for SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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54 TRIDEANQRATKMLGSG 70

2 TRIDEANQRATKMLGSG 18

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APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
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COUNTRY: USA
ZIP: 20005-3934
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE OF THE TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: PCT/GB95/01279
PILING DATE: 30-DECT W.
NAME: Esmond, RODERT W.
NAME: Esmond, RODERT W.
REGISTRATION NUMBER: 32,893
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; Sequence 11, Application US/09962360B

; Patent No. 6762280

; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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TELEFAX: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-819-286-1
                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
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                                                                                                                                                                                                                                                                                                                                         Length 116,
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                                                                                                                                                                                                                                                             , OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine US-09-962-360B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 84; DB 2; I
100.0%; Pred. No. 4.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08393985
; Sequence 18, Application US/08393985
; Patent No. 5693470;
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Composition, TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION UNMER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
ELNGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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CLASSIPICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFRENCE/DOCKET NUMBER: 8600-0152
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 TRIDEANQRATKMLGSG 115
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                                                                                                                                       TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 206 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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Matches 17; Conservative
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                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
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US-08-393-985-18
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190 TRIDEANQRATKMLGSG 206

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APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridistrine OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridistrine OF INVENTION: Neurotoxins
FILE REPERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR PILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 8
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08743894B

Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: Names J. Schmidt
APPLICANT: Karen A. Bostian
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn.John Moran-Patent Atty
STREET USA MRMC - 504 Scott Street
STATE: MAXYLAND
STATE: MAXYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT A PRATURE:
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                                                                                                                                                                               Length 116;
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          ; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature; LOCATION: 1; COCATION: 1; OTHER INFORMATION: Xaa at 1 is N-fluresceinyl-glycine; 03-09-962-3608-8
                                                                                                                                                                            Score 78; DB 2; 1
Pred, No. 5.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09962360B Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                  99 TRIDEANQAATKMLGSG 115
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                                                                                                                                                                                  92.9%;
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ORGANISM: Artificial sequence
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OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TRIDEANQRATRMLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schmidt, James J.
                                                                                                                                                                                      Query Match
Best Local Similarity 94.1<sup>†</sup>
Matches 16; Conservative
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nes 15; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-743-894B-1
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US-09-962-360B-8
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APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
FILE REFERENCE: 003/224/SAP
FILE REPERENCE: 003/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-94-016-10671
Sequence 10671, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WHERE: US/09/949,016
TITLE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REPERENCE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PILING DATE: 2000-10-20
FRIOR PILING DATE: 2000-10-20
FRIOR PILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 20012
SEQ ID NO 10671
LENGTHARE: FREESE for Windows Version 4.0
SEQ ID NO 10671
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                                                                                                                                                                                                                        100.0%; Score 84; DB 2; Length 206; 100.0%; Pred. No. 9.1e-07;
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100.0%; Score 84; DB
Best Local Similarity 100.0%; Pred. No. 9.8
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                           0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6311
LENGTH: 206
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Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 TRIDEANQRATKMLGSG 219
                                                                                                                                                                                                                                                                                                                                                                                                       190 TRIDEANORATKWLGSG 206
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-09-949-016-10671
                                                                                                                                   ; ORGANISM: Human
US-09-949-016-6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-962-360B-12
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Query Match

81.0%; Score 68; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 3, 2006, 15:33:15 Job time : 15.1651 secs
                                                                                                                                                                                                                                                                                                                             2 TRIDEANORATKML 15
                                                                                                                                                                                                                                                                                                                                                                                                     4 TRIDEANORATKML 17
                                                        ; FEATURE:
US-08-743-894B-37
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Setting 1.0
Setting 3.7
Setting 
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Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches Λ. τ-Δ-1-
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
RAPLICATION A15
PROR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT: INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 134,616
REGISTRATION NUMBER: 15-0055
TELEFAN: (301) 619-2065
TELEFAN: (301) 619-714
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Allear
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ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFRAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTREISTICS:
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TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
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US-08-743-894B-37
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
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096814_MACRA
096814_MACRA
080758_CARAU
093579_BRARE
080757_BRARE
SN25A_CARAU
0705J6_LATJA
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Maximum Match 100%
Listing first 45 summaries
                                                                                         protein search, using sw model
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QSNVK3_
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Perfect score:
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Q661d7 brachydanio
Q4v9b7 brachydanio
Q4v9b brachydanio
Q4v9b brachydanio
Q4v9b torpedo mar
Q8134 loligo peal
Q4rep6 tetraodon n
Q81187 xenopus lae
Q8636 lymnaea sta
Q98596 lymnaea sta
Q9xzj3 dictyostelli
Q9fje6 arabidopsis
P1104 spinacia ol
Q85431 pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINE MERGHALAL ALINGAGE. 73 (1998).

TO NOUNCOSCI. RES. 54 5:63 -573 (1998).

TO NOUNCOSCI. RES. 54 5:63 -573 (1998).

TO NOUNCOSCI. RES. 54 5:63 -573 (1998).

TO SAME, APO15. 1 1.4A.

TO SAME AP
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 26, Last annotation update)
8ynaptosome-associated protein 25.1 (Fragment).
Name-snap22a; Synonyms=2nap;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Cyprinidae; Danio.
NCBL TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDILTE=99057281, PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-UNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
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100.0%; Pred. No. 4.4e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AA
    0661D7_BRARE
0409B7_BRARE
0409B6_BRARE
SNP25_TORMA
081354_LOLD-BE
0401S7_XENLA
0801S7_XENLA
0801S7_XENLA
0805G6_LYMST
0985G6_LYMST
0985G6_LYMST
0985G6_BRATH
0987B6_ARATH
0987B6_ARATH
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085439 PSEFL
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093578;
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
TISSUB-Brain parietal lobe;
TISSUB-Brain parietal lobe;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                         Tetracdon nigroviridis (Green puffer).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Etrinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetracdontiformes,
Tetradontoidea, Tetracdontidae, Tetracodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macakaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                           13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14706, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FBB-2004) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; CAAE01014706; CAG03117.1; -; Genomic DNA.

EMBL; CAAE01014706; CAG03117.1; -; Genomic DNA.
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EMBL; AB049852; BAB16738.1; -; mRNA.
HSSP; Q8T3S4; 1L4A.
                         134 AA
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Nature 431:946-957(2004).
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                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
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                                                                                                                                                                          ORFNames=GSTENG00022427001;
                 Q4S8B5_TETNG PRELIMINARY;
Q4S8B5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GM34 MACFA PRELIMINARY;
Q9GM34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ibraries.";
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NUCECTION SEQUENCE.

STRAIN-Wild-type; TISSUG-Eye;

NUCECTION SEQUENCE.

STRAIN-Wild-type; TISSUG-Eye;

NUCECTION SEQUENCE.

STRAIN-Wild-type; TISSUG-Eye;

NEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rach J., Helton B., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriquez A.C., Grimwood J., Schmutz J., Whyers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rodereztion and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei, Ostarlophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
X SME; Q9GM34; 68-141.

R GO; GO:0019717; C:synaptosome; IEA.

R InterPro; IPR000228; SNAP-25.

R InterPro; IPR000727; T. SNARE.

R Pfam; PF00835; SNAP-25; 1.

R Pfam; PF005739; SNARE; 1.

R Pfam; PF005739; L. SNARE; 1.

DR RMST; SW00397; L. SNARE; 1.

DR PROSITE; PS50192; T. SNARE; 1.

KW HYDOThetical protein; Synaptosome.

KW HYDOTHETICAL BAA; 16043 MW; D625DBAAA0893FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strauberg R.;
Strauberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOS9439; AAHS9439.1; -; mRNA.
SNR; OSFC84; 1-77, 123-196.
ZFIN; ZDB-GENE-980526-468; snap25a.
CG) GO:019171; C:Synaptosome; IEA.
InterPro; IPR000727; T_SNARE.
Pfam; PF06035; SNAP-25;
InterPro; IPR00035; SNARE.
Pfam; PF05739; SNARE; 1.
SNARE; L_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGPC84 BRARE PRELIMINARY; PRT; 198 AA.
QGPC84;
QGPC84;
GGPC3-U1L-2004 (TrEMBLrel. 27, Created)
05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 84; DB 2; I
100.0%; Pred. No. 5.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 TRIDEANORATKMLGSG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TRIDEANQRATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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18

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2 TRIDEANQRATKMLGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synaptosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R EMBL; L22976; AAA16538.1; -; mRNA.

R HSSP; P13795; LSPC.

R SMR; P13795; LSPC.

R SMR; P136978; 7-82, 128-201.

R InterPro; IPR000928; SNAP-25.

R Dfam; PF005739; SNARE; 1.

R Pfam; PF05739; SNARE; 1.

R RART; SM00397; L SNARE; 2.

R ROSITE; PS50192; T SNARE; 2.

R Coiled coil; Glycoptrein; Multigene family; Repeat; Synaptosome.

T DOMAIN 19 81 t-SNARE coiled-coil homology 1.

T SOMAIN 137 199 t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carassius auratus (Goldfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Carassius.

NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
-1- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cereballum.
-!- SIMILARITY: Belongs to the SNAP-25 family.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cys-rich.
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
SPERBERBERD37D6D7 CRC64;
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Risinger C., Larhammar D.; "Multiple loci for synapse protein SNAP-25 in the tetraploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 84; DB 1; Length 203; 100.0%; Pred. No. 7.3e-06;
                                                                          Length 198;
                                                                                                                         Indels
                           22209 MW; 8FED5099A00E1EC0 CRC64;
                                                                       / Match 100.0%; Score 84; DB 2; Lv
Local Similarity 100.0%; Pred. No. 7.1e-06;
nes 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
110-MAY-205 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25B (SNAP-25B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                              203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94068448; PubMed=8248151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22664 MW;
                                                                                                                                                                                                           182 TRIDEANORATKMLGSG 198
                                                                                                                                                                           2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nerve terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                  198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Retina;
              Synaptosome.
                                                                                                                                                                                                                                                                                                                                                 CARAU
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                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    goldfish
                                                                               Query Match
                                                                                                                                Matches
                                                                                                                                                                                                                                                                                               RESULT
SN25B C
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comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage."; J. Neurosci. Res. 54:563-573(1998).
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Buschydanio metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
                                                                                                                                               Name=snap25b; Synonyms=Snap;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Wild-type; TISSUE-Eye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning of two loci for synapse protein Snap25 in zebrafish:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 84; DB 2; Length 203; 100.0%; Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6PC547
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Synaptosome-associated protein 25.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 AA
203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synaptosome-associated protein 25 b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF091594; AAC64290.1; -; mRNA.
HSSP; P608B1; 1JTH.
HSSP; O93579; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 TRIDEANORATKWLGSG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRIDEANORATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SYMADCAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00835; SNAP-25; 1. Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEPC54_BRARE PRELIMINARY;
O93579 BRARE PRELIMINARY;
093579;
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Gaps

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Indels

17; Conservative

Matches

Best Local Similarity

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COMPBIAS
SEQUENCE
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                                                                      removed
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hesieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brans S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garzente P.H., A Richards S., Worley K.C., Hale S., Garzente B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ablakealey R.W., Touchman J.W., Green E.D., Dickson M.C., A Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Topheration and initial amalysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carassius auratus (Goldfish).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
--- PUNCTION: May play an importent role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the nerve terminal. SIMILARITY: Belongs to the SNAP-25 family. SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Retina;
MEDIJNE=94068448; PubMed=8248151;
Risinger C., Laxhammar D.;
"Multiple loci for synapse protein SNAP-25 in the tetraploid
goldfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 84; DB 2; Length 203; ; Pred. No. 7.3e-06; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                (OCT-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                          203 AA; 22693 MW; 48D7590DD0C1179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-Rel. 29, Last annotation update)
Synaptosomal-associated protein 25A (SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AA.
                                                                                                                                                                                                                                                                                         EMB1, BC059469, AAH59469.11 - ; mRNA. SNR, Q6PC54; 7-82, 128-201.
STRN, 2DB-GENE-990526-392; enap25b. GO; GO:0019717; C:synaptosome; IEA. InterPro; IPR000928; SNAP-25. Pfan; PF00835; SNAP-25. Pfan; PF00835; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 TRIDEANQRATKMLGSG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                        STRAIN=Wild-type; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
Best 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                    Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARAU
                                                                                                                                                                                                                                                                                                                                                                                                                               Synaptoвоше
                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REC.
SN25A CAL.
ID SN25A CAL
P36977;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
A Chen K., Huang X.H.;
A Chen K., Huang X.H.;
Submitted (DEC_2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; AJ61993; CAP04071.1; -; mRNA.
R GO; GO:00003700; F:transcription factor activity; IEA.
GO; GO:00003700; F:transcription of transcription, DNA-dependent; IEA.
R GO; GO:000035; SNAP-25.
R InterPro; IPR000727; T_SNARE.
R Pfam; PF05739; SNARE; 1.
R Pfam; PF05739; SNARE; 1.
R SMART; SM00397; T_SNARE; 2.
R SMART; SM00397; T_SNARE; 2.
R ROSITE; PS50192; T_SNARE; 2.
R SRQUENCE 204 AA; _22842 MW; BF77B1BD591509B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                  R EMBL; L22973; AAA16537.1; -; mRNA.
R H7SP; P1395; L130480.
R H7SP; P1395; L130480.
R RR; P36977; 7-83, L29-202.
R InterPro; IPR000928; SNAP-25.
R InterPro; IPR000727; T SNARE.
R Fam; PF00835; SNAP-25; 1.
R Pfam; PF00739; SNARE; 1.
R PROSITE; PS50192; T SNARE; 2.
R PROMAIN 138 200 t-SNARE coiled-coil homology 1.
I DOMAIN 138 200 t-SNARE coiled-coil homology 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 84; DB 2; Length 204; 100.0%; Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458BBECFCFC09189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Synaptosomal-associated protein 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 84; DB 1; I 100.0%; Pred. No. 7.3e-06; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 92 C
204 AA; 22843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 TRIDEANORATKWLGSG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TRIDEANORATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q705J6 LATJA PRELIMINARY;
Q705J6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
85
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EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P60878-2, P13795-2;
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                                                                                                                                                                                                                                                                                                            188 TRIDEANORATKMLGSG 204
                                                                                                                                                                                                                                                                                 2 TRIDEANORATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence=Displayed;
Name=SNAP-25a;
                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=SNAP-25b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson M.C.;
                                                                                                                                                                           Synaptosome
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Synaptosomal-associated protein (SNAP).
Name=snap25a; Synonyms=OTTDARP0000005690; ORFNames=DKEYP-8F4.6-002;
Brachydaino rerio (Zebrafish) (Danio rerio).
Brachydain, Metacoa; Chordain; Canniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                              01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
Synaptosomal-associated protein (SNAP).
Name=snap25a; Synonyms=OTTDARP0000005563; ORFNames=DKEYP-8F4.6-001;
Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 84; DB 2; Length 204; Local Similarity 100.0%; Pred. No. 7.3e-06; Nes 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               Donaldson S.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX465184; CAH69031.1; -; Genomic_DNA.
REMBL; BX470246; CAH69031.1; JOINED; Genomic_DNA.
REMBL; BX470246; CAH69031.1; JOINED; Genomic_DNA.
REMBL; BX465184; CAL51359.1; JOINED; Genomic_DNA.
REMBL; BX465184; CAL51359.1; JOINED; Genomic_DNA.
REMBL; BX465184; CAH59031.1; JOINED; Genomic_DNA.
REMBL; BX400020609; Danio rerio.
R ZFIN; ZDB-GENB-980526-468; SNAPE.3.
R InterPro; IPR000228; SNAPE-25.
R InterPro; IPR000228; SNAPE-25.
R Ffam; PP003739; SNARE; 1.
R SMART; SM00397; t_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Donaldson S.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, Bx465184; CAH69032.1; -; Genomic_DNA.
EMBL, Bx470246; CAIZ1360.1; -; Genomic_DNA.
EMBL, Bx470246; CAIZ1360.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lovell J.; Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                       Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
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                                    204 AA
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                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSTZ65_BRARE PRELIMINARY;
                                   QSTZ66 BRARE PRELIMINARY;
QSTZ66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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셤 8

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Event=Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP25 CHICK STANDARD; PRT; 206 AA.

ID SNP25 CHICK STANDARD; PRT; 206 AA.

OF 60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;

DT 01-JRA-1990 (Rel. 13, Created)

DT 01-FB-1991 (Rel. 17, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

E Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated BD Synaptosomal-associated protein (SUP).

OS Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STXIA. This complex binds CPLXI. Interacts with TRIM9, RIMS1 and SNAP25BP. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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J. Mol. Biol. 233:67-76(1993).
-!- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-White leghorn, TISSUE-Retina,
MEDLINE-91126080, PubMed=1992470,
Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of a conserved cell-type-specific protein in nerve terminals coincides with synaptogenesis."; Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 84; DB 2; Length 204; 100.0%; Pred. No. 7.3e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B)
MEDLINE-93389738; PubMed=8377193;
SMR; Q5TZ65; 7-83, 129-202.
Ensembl; ENSDARGO000020609; Danio rerio.
ZFIN; ZDB-GENE-990526-468; Enap25a.
GO; GO: 0019717; C:8yraptcosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR00777; T. SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF00739; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
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removed

EMBL;

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NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B)
                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A)
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                                        Bark I.C., Wilson M.C.;
                                                                                                                        rissum=Brain;
                                                                                                                                                                                                                                                                      Ward C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rogers J.,
  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                        the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cys-rich.
Cleavage (by BONT/E) (By similarity).
Phosphothreonine (By similarity).
Phosphoscrine (By similarity).
ERIEEGMDQINKDMKEAEKNLTDLGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMNHINQDMKEAEKNLKDLGKCCGLFI (in isoform
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t-SNARE coiled-coil homology 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84; DB 1; Length 206; Pred. No. 7.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00397; t.SMARE; 2.
PROSITE; PS50192; T. SNARE; 2.
Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VSP 010018.
FBED28082A4CB6A6 CRC64;
                                                                                                                                                                      | AAA49070.1; JOINED; Genomic DNA. | AAA49071.1; JOINED; Genomic DNA. |
                                                                                                                                                                                                                                                                                 L09259; AAA49071.1; JOINED; Genomic_DNA.
L09252; AAA49071.1; JOINED; Genomic_DNA.
L09252; AAA49071.1; JOINED; Genomic_DNA.
L09258; AAA49071.1; JOINED; Genomic_DNA.
L09250; AAA49071.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                EMBL; M57957; AAA49072.1; -; mRNA.
EMBL; L09253; AAA49070.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNAP-25a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation, Repeat; Synaptosome.
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0
                                                                                                                                                                                                                                                                                                                                                  PIR, A37861, A37861.
SMR; B60878; 7-83, 131-204.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 TRIDEANORATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 AA; 23315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100. es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                     L09259;
                                                                                                                                                                                                                    L09251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPBIAS
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DOMAIN

Best Loc Matches

RESULT 13

EMBL; EMBL;

\$\frac{1}{2}\frac{1}\frac{1}{2}\f

EMBL; EMBL; EMBL; EMBL; EMBL;

EMBL; EMBL;

EMBL;

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RX MUCLECATIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MUCLECATIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX DELOUKAS P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Baley J., Barlow K.F., Bates K.M., Beard L.M., Beare D.M.,

Basley O.P., Bid C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Back D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Ellington A.G., Frankland J.A., Perast D.D., Gwilliam R., Hall R.E.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA HARLEY J.L., Heath P.D., Ho S., Holden J.L., Jowden P.J.,

RA Lebraselaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lowell J.D.,

RA Mins S.L., Mistry D., Moore M.J.E., Mullikin J.C., Nickerson T.,

RA Milne S.L., Ratherlingam S.R., Plumb R.W., Ramsay H.,

RA Swamor R.M., Sycamora N., Patell R., Pearce T.A.V., Peck A.I.,

RA Swamor R.N., Scott C.E., Sehra H.K., Shownkeen R., Sins S.,

RA Swamor R.N., Sycamora N., Taylor R., Thomas D.W., Thorpe A.,

RA Swam R.M., Sycamora N., Taylor R., Thomas D.W., Thorpe A.,

RA Wiltehead S.L., Whittaker P., Willey D.L., Williams S.A.,

RA ROOFF J., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA ROOFF J., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUREEPS;

X REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klauener R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Skeletal muscle;
MEDLINE-96332494; PubMed-8760387;
Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
Biochem. J. 317:945-954 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9433329; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2; Zhao N., Hashida H., Takahashi N., Sakaki Y.; "Cloning and sequence analysis of the human SNAP25 cDNA."; Gene 145:313-314(1994).
MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
                                                                                                  "Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25."; Gene 139:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
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EMBL; AL022913; CAC34534.1; -; Genomic DNA.
EMBL; AL023913; CAC34535.1; -; Genomic DNA.
EMBL; AL023913; CAD56158.1; -; Genomic DNA.
EMBL; AL023913; CAB42860.1; -; Genomic DNA.
EMBL; BC010647; AAH10647.1; -; Genomic DNA.
PIR; I53735; I53735.
PIR; I67823; I67823.
                                                                                                                                                                                                                                                                                                                                                                                                                             mbl; ENSG0000132639; Homo sapiens
; HGNC:11132; SNAP25.
                                                                                                                                                                                                                                                                                                                                                                                                  1KIL; K.ray; C=11-80, D=141-203.
1KTG; K.ray; B=146-204.
P60880; 7-83, 131-204.
                                                                                                                                                                                                                                                                                                                               EMBL; L19760; AAC37545.1; -; mRNA.
EMBL; L19761; AAC37546.1; -; mRNA.
EMBL; D21267; BAA22370.1; -; mRNA.
                                                                                                                                                                                                       IsoId=P60880-1, P13795-1;
                                                                                                                                                                                                               Sequence=Displayed;
                                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC; HGNC:11132; SNA
H-InvDB; HIXO015639;
MIM; 600322; -.
                                                                                                                                                                                                  Name=SNAP-25b;
                                                                                                                                                                                                                                                                                                                                                                                                                        IntAct; P60880;
                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl;
                                                                                                                                                                                                                                                                                                                    removed
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                                                                                                                                                                                                                                                                                                                                                                                                                  SMR;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                      Cys-rich.
Cleavage (by BONT/E).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
ERIEEGMDQINKOMKEAEKNLTDLGKECGLCV.->_ DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP35 MACMU STANDARD; PRT; 206 AA.
P60877; P13795; P36974; P70559; Q8IXK3; Q96FM2; Q9BR45;
01-JAN-1990 (Rel. 13, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
13-SEB-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eliminarity).

-!-SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2, and STXIA. This complex binds CPLXI. Interacts with TRIM9, RIMS1, SNAP25RP and HGS. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity).
-!-PTM: Palaitoylated (By similarity).
-!-SIMILARITY: Belongs to the SNAP-25 family.
-!-SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                      GMNHINODMKEAEKNLKDLGKCGLFI (in isoform SNAP-25a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Hippocampus;
Jensem M.J., Smith L.A.;
Jensem M.J., Smith L.A.;
Jensem M.J., Smith L.A.;
Jensem M.G., Smith L.A.;
Jensem M.G., Smith L.A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: t-SNARE involved in the molecular regulation of
neurorizansmitter release. May play an important role in the
synaptic function of specific neuronal systems. Associates with
proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
Pfam; PF00835; SNAP-25; 1.
Fram; PF05739; SNARE; 1.
SNART; SM00397; t SNARE; 2.
PR051TE; PS50192; T SNARE; 2.
3D-structure; Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat; Synaptosome.
Palmitate; Phosphorylation; L-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 84; DB 1; Length 206; 100.0%; Pred. No. 7.4e-06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               7 82
142 201
202 202
206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_006186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 TRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMR; P60877; 7-83; 131-204.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
Les 17, Conservative
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                                                                                                                                                                                                                                                                                     MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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HELIX
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                                                                                                                                                                                                          **RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX WITH STX1A; CPLX1 AND VAMP2, AND NWR ANALYSIS.

**MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273 (02) 00583-4; Chen X., Tomchick D.R., Kovrigin B., Arac D., Machius M.,

**Chen X., Tomchick D.R., Kovrigin B., Arac D., Machius M.,

**Suedhof T.C., Rizo J.;

**Three-dimensional structure of the complexin/SNARE complex.";

**Neuron 33:397-409(2002)

**Intere-dimensional structure of the molecular regulation of neurotransmitter release. May play an important role in the neurotransmitter release. May play an important role in the proteins involved in vesicle docking and membrane fusion.

**PUBMIT: Part of the SNARE core complex containing SNARPS; VAMP2

**And STXIA. This complex binds CPLXI. Interacts with TRIM9, RIM51, SNARPSSEP and HGS. Binds STXRP6. Found in a ternary complex with analyzants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
                                                  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO: 00007269; P:neurotransmitter secretion; NAS.
GO; GO:0001504; P:neurotransmitter uptake; NAS.
GO; GO:0001504; P:neurotransmitter uptake; NAS.
GO; GO:0007268; P:regulation of insulin secretion; TAS.
GO; GO:0016081; P:synaptic transmission; NAS.
GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8IUH5:HIP14; NbExp=1; IntAct=EBI-524785, EBI-524753;
                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Gaps

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STRAIN=C57BL/6J; TISSUE-Medulla oblongata;

X MEDLINE-223546681; PUMPAGE 1.0 1038/nature01266;

Nikaido I., Osato N., Kaukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Manapin A., Matsuda H., Batalov S., Baisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Blake J.A., Pletcher C.F., Forrest A., Frazer K.S.,

A Gasaterland T., Gariboldi M., Gissi C., Godzik A., Guugh J.,

A Kanai A., Kawasii H., Kawasawa Y., Kedzierski R.M., King B.L.,

A Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
                                                                                                                                                                                                                                                                                                                  SNP55 MOUSE STANDARD; PRT; 206 AA.
P60875; P13795; P36974; P70557; P70558; QBIXK3; Q96FM2; Q9BR45;
D1-JAW-1990 (Rel. 13, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated arsociated protein) (SUP).
Mame-Snap25; Synonyms-Snap;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M., Bloom P.E., Wilson M.C.;
"The identification of a novel synaptosomal-associated protein, SNAP-25, differentially expressed by neuronal subpopulations.";
                                                                                                                                                                                                       Gaps
                                                                                                             Cleavage (by BONT/E) (By similarity). Phosphothreonine (By similarity). Phosphoserine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ILS, and ISS;

BABLINE-2163810; PubMed=11471062; DOI=10.1007/s00335-001-1001-x;

Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,

Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;

"High-throughput sequence identification of gene coding variants

within alcohol-related GTHs.";

Mamm. Genome 12:657-663 (2001).
                                                                                                                                                                                                       ö
                     SMART, SM0397; t SNARE; 2.
PROSITE; PS50192; T SNARE; 2.
Colled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
                                                                      t-SNARE coiled-coil homology 1.
t-SNARE coiled-coil homology 2.
Cys-rich.
                                                                                                                                                                             Length 206;
                                                                                                                                                                                                      0; Indels
                                                                                                                                                  FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                             Score 84; DB 1; I
Pred. No. 7.4e-06;
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                        190 TRIDEANQRATKMLGSG 206
                                                                                                                                                     23315 MW;
                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                2 TRIDEANQRATKWLGSG 18
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                          81
202
92
181
138
138
                                                                                                                                                   206 AA;
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                                                               Synaptosome.
                                                                                      DOMAIN
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MOD RES
SEQUENCE
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NECESTIDE SEQUENCE LLARGE SCALE MENA) (150FORM SNAP-25A).

STRAIN-C57BL/6: TISSUB-Eye;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L.; Feingold B.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A. Michard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Pahey J., Helton B.K., Kuremen M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,

B. Mining M., Madan A., Schein J.B., Jones S.J.M., Marra M.A.;

Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,

B. Manner D. M., Machan J. W., Marra M.A.;

Beneration and initial analysis of more than 15,000 full-length human
Petrovsky N., Fillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setcou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Sultana R., Savolan M., Taylor M.S., Teasdale R.D., Tomita M.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
Wann Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Ahra A., Hashizume W., Indrani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Rasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing, Named isoforms=2, Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3; Hepp R., Cabaniols J.P., Roche P.A.; "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with protein involved in vesicle docking and membrane fusion. SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STAXA. This complex binds CPLAI. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STABB6. Found in a ternary complex with STAIA and VAMP8 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 512:52-56(2002).
-!- FUNCTION: t-SNARE involved in the molecular regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pubmed=10195194; DOI=10.1038/5673;
flardi J.M., Mochida S., Sheng Z.-H.;
Snapin: a SNARE-associated protein implicated in synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION SITES THR-138 AND SER-187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P60879-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Neurosci. 2:119-124(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=SNAP-25b;
IsoId=P60879-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH SNAP25BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence=VSP_010019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmission.
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CC --- SIMILARITY: Belongs to the SMAP-25 family.
--- SIMILARITY: Belongs to the SMAP-25 family.
--- SIMILARITY: Enclode to the SMAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
--- CC the small coiled by the SMALOND COILED by SMALOND COIL --- MANA.
--- DR EMBL, AR493516, AAL9079011: --- MANA.
--- DR EMBL, AR493516, AAL9079011: --- MANA.
--- DR EMBL, AR493516, AAL907011: --- MANA.
--- DR EMBL, AR493516, AAL9070011: --- MANA.
--- DR EMBL, AR493517, AAL9070011: --- MANA.
--- DR EMBL, AR7070011: --- MANA.
--- DR EMBL, AR707001: --- MANA
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Db 190 TRÍDEANÓRATKMIGSG 206 Search completed: April 3, 2006, 15:46:26 Job time : 98.9633 secs

2 TRIDEANORATKMLGSG 18

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 3, 2006, 15:30:10 ; Search time 10.2844 Seconds (without alignments) 177.756 Million cell updates/sec

US-09-942-098-92 84 Title: Perfect score:

1 XTRIDEANQRATKMLGSGX 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		٠			SUPERKIES	
Result	9	Query	Length	ä	1	Description
2	1000			} ;		
-1	84	100.0	203	7	I50481	
7	84	100.0	204	~	I50480	synapse protein SN
m	84	100.0	206	N	A37861	synaptosomal-assoc
4	84	100.0	206	N	153735	nerve terminal pro
S	84	100.0	206	7	167823	nerve terminal pro
9	84	100.0	206	7	A33623	synaptosomal-assoc
7	54	64.3		~	I50552	synapse protein -
80	48	57.1	29	~	A49708	synaptosomal-assoc
0	46	54.8	1361	~	A29959	DNA-directed RNA p
10	45	53.6	296	N	D87525	conserved hypothet
11	44	52.4	278	~	AH3356	comE operon protei
12	44	52.4	1578	~	876238	hypothetical prote
13	42	50.0		~	A33854	outer membrane lip
14	4	50.0	-	~	T33167	hypothetical prote
15	41	48.8		7	JC5297	vesicle-membrane f
16	41	48.8		~	JC5512	SNARE protein 23 -
17	41	48.8	211	~	JC5296	×
18	41	48.8		~	T23869	
19	41	48.8		N	T29386	
20	41	48.8	2288	N	T29999	hypothetical prote
21	40	47.6		•	S77848	probable valine-tR
22	40	47.6		N	AD2473	٠.
23	40	47.6		•	G71563	_
24	40	•		~	T34187	_
25	40	47.6		~	T52524	_
56	40	47.6	642	N	G90551	lipoprotein (impor
27	40	47.6	7	7	G75477	യ
28	39	46.4		~	A69282	۲ũ.
29	39	46.4	241	-	RRNZ	phosphoprotein P -

phosphoprotein P - rod shape-determin	NAD(P)H-dependent lybyl-tRNA synthet	hemagglutinin-neur hemagglutinin-neur	hemagglutinin-neur	hemagglutinin-neur	hemagglutinin-neur	hypothetical prote	lcrD protein - Yer	dynein heavy chain	hypothetical prote	genome polyprotein	hypothetical prote	hypothetical prote
RRNZPP A82325	H83854 C87259	G46328	E46328	F46328	HNNZNC	T48697	\$25586	T34340	T16613	JQ1303	T35151	н85061
7 7	0 0	٦.		н	-	N	N	N	N	н	~	0
241 296	345	577	577	577	577	602	704	1198	2427	3033	461	1196
46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	45.8	45.8
6 E	თ თ ო ო	000	9 6	39	39	39	39	39	39	39	38.5	38.5
30 31	32	1 60 c	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 150481 8ynapse C;Specie C;Date: C;Access	RESULT 1 150481 synapse protein SNAP-25 - goldfish C;bpcies: Carassius auratus (goldfish) C;bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 C;Accession: 150481 R;Risinger, C.; Larhammar, D.
Proc. I	Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title	A;Fitle: Multiple loci for Bynapse protein SNAP-25 in the tetraploid goldfish.
A;Refe	A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Stati	A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Mole	A;Molecule type: mRNA
A;Residues:	A,Residues: 1-203 <ris></ris>
A;Cross-ref	A,Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:g349430; PIDN:F
C;Genetics:	C,Genetics:
A;Gene: SNA	A,Gene: SNAP-25
Quer	Query Match
Best	Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matci	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ò	2 TRIDEANQRATKMLGSG 18
q	187 TRIDEANQRATKMLGSG 203

synapse protein SNAP-25 - goldfish
Syperies: Carassius auratus (goldfish)
C;Species: Carassius auratus (goldfish)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: 150480
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Residues: 1-204 <RIS>
A;Genetics: C;Genetics: A;Genetics: A;Genetic

/ Match 100.0%; Score 84; DB 2; Length 204; Local Similarity 100.0%; Pred. No. 2.4e-07; nes 17; Conservative 0; Mismatches 0; Indels 2 TRIDEANORATIONLGSG 18 Query Match Best Local S: Matches 17, g ò

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Gaps

Accession: A37861

RESULT 3

Match 100.0%; Score 84; DB 2; L Local Similarity 100.0%; Pred. No. 2.4e-07; les 17; Conservative 0; Mismatches 0;

Best Loca Matches

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Synapse protein - marbled electric ray
Gypecies: Torpedo marmorata (marbled electric ray)
C;Species: Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: S6552
B;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V./
J. Biol. Chem. 266, 24408-24414, 1993
A;Reference number: A49513; MUID:94042281; PMID:8226991
A;Reference number: A49513; MUID:9404281; PMID:8226991
A;Accession: I50552
A;Accession: I50552
A;Accession: L50552
A;Residues: L-210 <RIS>
A;Residues: L-210 <RIS>
A;Residues: L-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UP10000135AFE; GB:L22020; NID:g431296; PIDN:}
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Crispecies: Rattus norvegicus (Norway rat)
Crispecies: Rattus norvegicus (Norway rat)
Crispecies: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
Criscossion: A49708
Ribinz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; h
Ribinz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; h
Ribinz, T.; Croteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; V. J. Cell Biol. 109, 3039-3052, 198
A;Fitle: The identification of a novel synaptosomal-associated protein, SNAP-25, differer A;Reference number: A33623; MUID:90078337; PMID:2592413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNĀ
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI000001103; GB:M22012; GB:X51673; NID:g200
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                                                                                                             Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                      Query Match 100.0%; Score 84; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.3%; Score 54; DB 2; Best Local Similarity 84.6%; Pred. No. 0.057; Matches 11; Conservative 1; Mismatches
A,Cross-references: GDB:155671; OMIM:600322
A,Map position: 20p11.2-20p11.2
                                                                                                                                                                                                                                                                                                                             190 TRIDEANORATKWLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 TRIDEANQRATKMLGSG 206
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198 RIDEANKHATKML 210
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R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein A;Reference number: 153735; MUD: 94156217; PMID: 8112622
A;Accession: 153735
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-206 <RES>
A;Residues: 1-206 <RES>
A;Cross.references: UNIPROT: P60880; UNIPARC: UPIO00002B3DD; GB: L19760; NID: g307425; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 167823
R;Bark, I.C.; Wilson, M.C.
R;Bark, I.C.; Wilson, M.C.
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: 153735; MUID:94156217; PMID:8112622
                                                                                                                                                                                                                                                                                           R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C. Proc. Natl. Acad. Sci. US.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid A;Reference number: A37861; MUID:91126080; PMID:1992470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-206 <RES>
Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: A37861
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-206 <CAT>
A; Cross-references: UNIPROT: P60878; UNIPARC: UPI0000001103; GB:M57957; NID:G212673; PIDN:
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                                                                                                                                               synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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.Match 100.0%; Score 84; DB 2; I Local Similarity 100.0%; Pred. No. 2.4e-07; es 17; Conservative 0; Mismatches 0;

Query Match

2 TRIDEANQRATKMLGSG 18

A,Cross-references: GDB:355671; OMIM:600322 A,Map position: 20p11.2-20p11.2

A; Gene: GDB: SNAP

A,Accession: 167823 A,Status: preliminary; translated from GB/EMBL/DDBJ

Sene: GDB:SNAP

DB 2; 0.077;

Score 48; DB 2 Pred. No. 0.077 1; Mismatches

Query Match 57.1%; Best Local Similarity 62.5%; Matches 10; Conservative

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3 RIDEANORATKWLGSG 18

A,Status: preliminary A,Molecule type: protein A,Residuse: 1-29 «BIN» A,Cross-references: UNIPARC:UP1000017C9D4

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A;Cross-references: UNIPROT:P11221; UNIPARC:UPI000002C273; GB:M25761; NID:g151334; PIDN:
                                                                                                C;Accession: AH3356
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, B.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens; A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1578 <KAN>
A;Cross-references: UNIPROT:P74400; UNIPARC:UPI00000C10E9; EMBL:D90914; GB:AB001339; NID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dypothetical protein al10267 - Synechocystis sp. (strain PCC 6803)
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: S76238
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q8YHG3; UNIPARC:UPI0000057E30; GB:AE008917; PIDN:AAL52019.1;
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane lipoprotein I precursor - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33854; S04834; A48334; A83288
R;Duchene, M.; Barron, C.; Schweizer, A.; von Specht, B.U.; Domdey, H.
J. Bacteriol. 171, 4130-4137; 1989
A;Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning,
A;Reference number: A33854; MUID:89327122; PMID:2502533
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comB operon protein 3 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Fb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 4
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1004 QLDQANQRAQNQLG 1017
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Best Local Similarity 57.19
Matches 8; Conservative
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-278 < KUR>
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A; Residues: 1-83 < DUC>
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A, Gene: BMEI0838
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87525
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, K.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Fitle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Reaidues: 1-1361 <HUD>
A;Cross-references: UNIPROT:P11704; UNIPARC:UPI0000134774; EMBL:M55297; NID:G295119; PIC
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A;Cross-references: UNIPROT:Q9A665; UNIPARC:UPI00000C765E; GB:AE005673; NID:913423736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed RNA polymerase (EC 2.7.7.6) beta', chain - spinach chloroplast C; Species: chloroplast Spinacia oleracea (spinach)
C; Species: LS-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C; Accession: A29595
R; Hudson, G.S.; Holton, T.A.; Whitfeld, P.R.; Bottomley, W.
J. Mol. Biol. 200, 633-654, 1988
A; Title: Spinach chloroplast rpo8C genes encode three subunits of the chloroplast RNA A; Reference number: A29959; MUID:88316931; PMID:3045324
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                                                                                                                                                   Length 29
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RESULT 10

3 RIDEANQRATKMLGS 17

Query Match
Best Local Similarity 60.0°
Matches 9; Conservative

A, Genome: chloroplast

A;Gene: rpoC-2

A;Accession: A29959

RESULT 11

250

4 IDEANQRATKMLGSG 18

Score 45; DB 2; Pred. No. 3.4; 2; Mismatches

53.6%;

Query Match
Best Local Similarity 60.00
Best Local 9; Conservative

A;Status: preliminary

A; Molecule type: DNA

A; Gene: CC2229

Genetics

96

A; Molecule type: DNA A; Residues: 1-83 < COR>

A; Accession: A44834

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A;Cross-references: UNIPARC:UPI0000176113; GB:chr_IV; PIDN:AAC17555.1; PID:g3158511; GSPI
C;Genetics:
                                                                                                                           A;Map position: 4
A;Introns: 41/2; 197/1; 263/3; 294/3; 793/2; 865/2; 904/3
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: ÚC5297
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 ir A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5597
A;Accession: JC5597
A;Status: nucleic acid sequence not shown; translation not shown
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A; Residues: 1-158 <MOL>
A; Cross-references: UNIPROT: O00161; UNIPARC: UP1000002B3DC; GB: Y09568; NID: g1924943; PIDN: A; Experimental source: neutrophils
C; Comment: This protein is involved in regulating exocytosis in human neutrophils, a cent
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C,Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vesicle-membrane fusion protein SNAP-23B - human
                                                                                                                                                                                                                                                                  Query Match 50.0%;
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 RIDIANARAKKLIDS 158
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823 LEEANVRADKLLG 835
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Best Local Similarity 60.03
Matches 9; Conservative
                                                                                          A, Gene: CESP: T26C12.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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                  R;Cornells, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube Mol. Microbiol. 3, 421-428, 1989
A;Title: Cloning and analysis of the gene for the major outer membrane lipoprotein from A;Reference number: S04834; MUID:89313294; PMID:2473376
A;Accession: S04834
                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI000002C273; EMBL:X13748; NID:g45344; PIDN:CAA32013.1; PID A;Note: the authors translated the codon GAA for residue 78 as Gly R;Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R. J. Gen. Microbiol. 138, 733-741, 1992 A;Title: Specificity of the Pseudomonaa aeruginosa PAO1 lipoprotein I gene as a DNA prob A;Reference number: A44834; MUID:92268853; PMID:1588307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Status: preliminary
A Molecule type: DNA
A, Residues: 1-83 <SAL>
A, Cross-references: UNIPARC:UP1000002C273; GB:X58714; GB:S36066; NID:9433509; PIDN:CAA41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: PAO1
A;Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIP:103667)
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A,Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPARC:UPI000002C273; GB:AE004712; GB:AE004091; NID:g9948940; PIDN:
A,Experimental source: strain PAO1
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3, 2006, 15:31:25
Search completed: April Job time: 11.2844 secs
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C; Keywords: lipid binding; lipoprotein; membrane protein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-83/Product: lipoprotein I #status predicted <MAT>

A; Molecule type: DNA A; Residues: 1-83 <STO> A, Accession: A83288 A, Status: preliminary

Local Similarity 72.7 5 DEANORATKML 15

Best Loc Matches

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Query Match

A;Accession: T33167
A;Accession: T33167
A;Accession: T33167
A;Accession: T33167
A;Accession: T33167
A;Accession: T33167
A;Accession: UNIPROT: O61859; UNIPARC:UPI0000176113; EMBL:AF067623; PIDN:AAC17555.
A;Esidues: 1-1056 <GAT>
A;Esperimental source: strain Bristol N2; clone T26C12
A;Experimental source: strain Bristol N3; pMID:995; and www sanger.ac.uk/Projects/C_eleA;Accession: D88645

esidues: 1-1056 <STO

Status: preliminary Molecule type: DNA

hypothetical protein T26C12.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33167; D88645
R;Gattung, S.; Scheet, P.; Harper, M.
a;Description: The sequence of C. elegans cosmid T26C12.
A;Reference number: Z21296

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Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Modified-site
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Botulinum
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(without alignments)
85.675 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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Maximum DB seq length: 200000000
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	26 Mouse syn 98 Mouse SNA 98 Synaptoso 53 SNARE hom 52 SNARE hom 52 Human SNA 57 Rat VAMP- 57 Rat Prote 80 Rat Prote 88 Rat Prote
Aaw30097 Aar86823 Aab13159 Aab13159 Aao11104 Abw01715 Aaw1104 Abw01715 Aaw30103	Aaw43426 Aaw79198 Aaw00253 Aau00253 Aau36667 Aae36667 Aae36667 Aae36667 Aae36667
AAW30097 AAR86823 AAB1584 AAB13169 AEA15002 AAA15165 AAA11044 ABW01715 AEM149001	AAW43426 AAW00246 AAW00253 AAW00252 AAB36662 AAB36667 ADE54280 ADE54280
37 2 86 8 86 8 8114 9 9116 5 200 8 200 3 9 200 206 206 206 206 206 206 206 206 206	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	W W W W W A A A A A A A A A A A A A A A

ALIGNMENTS

/note= "DABCYL-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 95 in the sequence listing of the specification" 19 Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; Fret substrate peptide #11 used in the invention. Aoki KR Location/Qualifiers AAE36740 standard; peptide; 19 AA щ 22-AUG-2002; 2002WO-US027145. Steward LE, Fernandez-Salas 28-AUG-2001; 2001US-00942024

Example 1; Page 115; 168pp; English

The present invention relates to novel clostridium toxin substrates. The

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unich comprise a donor fluorophore, an acceptor having an absorbance which comprise a donor fluorophore, an acceptor having an absorbance became overlation sequence comprising a cleavage site, where contrained the donor fluorophore and a comprise and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including bacterial, baculoviral and yeast loxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples. They are useful to assay a samples in abeverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and cosmedics. The present sequence is fret unbatrate peptide used in the exemplification of the invention
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Sequence 19 AA;

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100.0%; Score 84; DB 6; Length 19; 100.0%; Pred. No. 1.6e-07;
                           0; Indels
                            0; Mismatches
                                                           2 TRIDEANORATKMLGSG 18
                                                                            17; Conservative
             Best Local Similarity
Matches 17; Conserv
 Query Match
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Gaps

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RESULT 2 AAE36737

AAE36737 standard; peptide; 19 AA. 07-AUG-2003 (first entry) AAE36737;

Fret substrate peptide #8 used in the invention.

Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; cosmetic.

Unidentified

/note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 92 in the sequence listing of the specification" Location/Qualifiers Key Modified-site

/note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 92 in the sequence listing of the Modified-site

specification"

WO2003020948-A2

13-MAR-2003

22-AUG-2002; 2002WO-US027145.

28-AUG-2001; 2001US-00942024

(ALLR) ALLERGAN INC.

Aoki KR; Fernandez-Salas E, Steward LE,

WPI; 2003-290198/28.

Botulinum serotype A/E substrate useful for assaying protease activity of

Fernandez-Salas E, Aoki KR;

(STEW/) STEWARD L E. (FERN/) FERNANDEZ-SALAS E.

(AOKI/) AOKI K R.

Steward LE,

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The present invention fracts to hove to the droit substrates which comprise a donor fluorophore, an acceptor having an absorbance which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT A or BONT/B recognition sequence comporising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including betulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including betuerial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having production and purification of clostridial toxin, to follow activity during production and purification of clostridial pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
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botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
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                                                                                                the present invention relates to novel clostridium toxin substrates. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridial toxin, protease activity, tetanus toxin, botulinum toxin, FRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRET substrate #6 to analyse proteolytic activity of botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 84; DB 6; Length 19; 100.0%; Pred. No. 1.6e-07; ive 0; Mismatches 0; Indels
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                                                            Example 1; Page 115; 168pp; English.
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Best Local Similarity 100...
Local 17; Conservative
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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 29; Opp; English
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(FERN/) FERNANDEZ-SALAS E.
                                                                                                                                                           Local Similarity 100.
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WPI; 2003-829791/77
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This sequence corresponds to residues 187-206 of the human 25 kD synaptosomal associated protein (SNAP-25), and is a inhibitory agent of the invention. The agents of the invention inhibit secretion of neurotransmitter from neuronal cells and is an excitation-secretory uncoupling peptide (I) of at least 20 amino acids (as) all of which correspond substantially to any one of AAW30097-W30102, or more generally correspond substantially to any one of AAW30097-W30102, or more generally correspond at a concentration of 10 microw, especially 0.25 microw, or lease (I) are used, as a replacement for Clostridium toxin, to inhibit release of neurotransmitters from synaptic vesicles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of the drug to neural cells provide targeted drug delivery, e.g. of substance P to brain timours for induction of apoptosis Unlike the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Excitation-secretory uncoupling peptide(s) for inhibiting nuscle neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells.
                                                                                                      100.0%; Score 84; DB 7; Length 19; 100.0%; Pred. No. 1.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurotransmitter secretion inhibitor #4.
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                                                                                                                 100.0%; *-
                                                                                                                                                                                                                                                                                                                                           AAW30100 standard; peptide; 20
                                                                                                                                                                                             2 TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                     TRIDEANQRATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US004393.
                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1998 (first entry)
                                                                                           Query Match
Best Local Similarity 100...
Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-479986/44.
                                                                       Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                       AAW30100;
                                                                                                                                                                                                                                                                                                        RESULT 5
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                                                    Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                       The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRET substrate #9 to analyse proteolytic activity of botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 84; DB 7; I
Pred. No. 1.6e-07;
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                                                                                                                                         Example 1; Page 29; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, lower doses or less frequent treatments are required

Length 20;

Score 84; DB 2; 1 Pred. No. 1.7e-07;

100.0%;

Query Match Best Local Similarity Sequence 20 AA;

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substrate peptide used in the exemplification of the invention
                              Sequence 22 AA;
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                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and about A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the profease activity of any clostridial toxin including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast lights, raw, cooked or processed foods, beverages, animal feed, soil
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 93 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret
                                                                                                                                                                                                                                                                                                                                                      /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 93 in the sequence listing of the specification"
                                                                                                                                                                                                                                          Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
  Gaps
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    Indels
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                                                                                                                                                                                                               Fret substrate peptide #9 used in the invention.
    Mismatches
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                                                                                                                              AAE36738 standard; peptide; 22 AA.
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                              2 TRIDEANQRATKMLGSG 18
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                                                 4 TRIDEANORATKMLGSG
                                                                                                                                                                                      (first entry)
    17; Conservative
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                                                                                                                                                                                                                                                                                                                                Key
Modified-site
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                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                    07-AUG-2003
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                                                                                                                                                                                                                                                                         cosmetic.
    Matches
                                                                                                   RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining clostridial toxin protease activity, by treating sample with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Tetramethylrhodamine labelled lysine; C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   RRET substrate #7 to analyse proteolytic activity of botulinum toxin.
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  Length 22
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                                              Indels
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100.0%; Pred. No. 1.9e-07;
iive 0; Mismatches 0;
100.0%; Score 84; DB 6; I
100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Fluoresceinated lysine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                         ABW01794 standard; peptide; 22 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteolytic activity of botulinum exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TRIDEANQRATKMLGSG 18
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                                                                                                                         5 TRIDEANORATKMLGSG
                                                                                              2 TRIDEANQRATKMLGSG
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Matches 17; Conservative
                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STEW) STEWARD L E.
(FERN/) FERNANDEZ-SALAS
(AOKI/) AOKI K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-829791/77.
Query Match
Best Local Similarity
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Modified-site
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                                                  Matches
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Gaps

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Indels

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Example 1; Page 115; 168pp; English.
       AAE36733 standard; peptide; 23 AA.
                                                                                                                 22-AUG-2002; 2002WO-US027145
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                                                                                                                                (ALLR ) ALLERGAN INC
                                                                                                                                              WPI; 2003-290198/28.
                                                                                                                                                                                                                                                         23 AA;
                                                                                                   WO2003020948-A2
                                                          Key
Modified-site
                                                                            Modified-site
                                                  Unidentified
                                                                                                                                        Steward LE,
                     07-AUG-2003
                                                                                                          13-MAR-2003
                                            cosmetic.
              AAE36733;
RESULT 8
   AAE36733
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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serctypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of bottuliuum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRET substrate #2 to analyse proteolytic activity of botulinum toxin.
  2e-07;
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                                                  Mismatches
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                       Pred. No.
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100.08; Pr.
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                                                                                                    2 TRIDEANQRATKMLGSG
                                                                                                                                              TRIDEANQRATKMLGSG
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Matches 17; Conservative
                       Best Local Similarity 100.
Matches 17; Conservative
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FERNANDEZ-SALAS
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                ABW01789;
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(FERN/)
                                                                                                                                                                                                                                                      RESULT 9
ABW01789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BoNI/A/B) substrates which comparise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a spectrum overlapping the emission spectrum of the donor fluorophore and a captor fluorophore and a captor fluorophore and a captor fluorophore and a captor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMPP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the procease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus conting (TeNT) in a sample including botulinum toxins of all serotypes and tetanus lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, consention, tissue samples and beverage or food samples, ray are useful to assay a sample from a human or animal, for egg, exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin, products and clostridial toxin products and present and the acceptor of clostridial toxin products and the acceptor of clostridial toxin products and the acceptor of clostridial toxin man are and to clostridial toxin man are acceptor or acceptor of clostridial toxin products and the acceptor of clostridial toxin products and parts are acceptor or acceptor of clostridial toxin products and products and products and products and products and acceptor acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               __note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 88 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clostridial toxin products
present sequence is fret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 88 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                      Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   including pharmaceuticals and cosmetics. The present sequence substrate peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                    Fret substrate peptide #4 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aoki KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fernandez-Salas E,
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Gaps ö 100.0%; Score 84; DB 7; Length 23; 100.0%; Pred. No. 2e-07; ive 0; Mismatches 0; Indels AAE36735 standard; peptide; 24 AA. RESULT 10 AAE36735 ID AAE36

100.0%; Score 84; DB 6; Length 23;

Query Match

23

7 TRIDEANQRATKMLGSG

RESULT 11 ABW01791

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmettics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay a sample from a human or animal, for clostridial toxin, to follow activity during production and purification of clostridial toxin and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 90 in the sequence listing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                  /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 90 in the sequence listing of the specification"
                                                                                                                                                      Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 84; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 2.1e-07; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                        Fret substrate peptide #6 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 115; 168pp; English.
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2002; 2002WO-US027145.
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                                                                (first entry)
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                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                               Unidentified
                                                                07-AUG-2003
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                                                                                                                                                                                                     cosmetic.
                    AAE36735
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Aoki KR;

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                                                                                                                                                                                                                                           "Tetramethylrhodamine labelled lysine; C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the
                                                                                                            Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                FRET substrate #4 to analyse proteolytic activity of botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 84; DB 7; Length 24; 100.0%; Pred. No. 2.1e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                             /note= "Fluoresceinated lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aoki KR
                                                                                                                                                                                    Location/Qualifiers
ABW01791 standard, peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30099 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 29; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TRIDEANORATKMLGSG 18
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                                                       12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (STEW/) STEWARD L E.
(FERN/) FERNANDEZ-SALAS
                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                          amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-829791/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (AOKI/) AOKI K R.
                                                                                                                                                                                                                                                                                        US2003143651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 AA;
                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                              Modified-site
                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                   31-JUL-2003.
                            ABW01791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW30099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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ID AAW3
XX
AC AAW3
XX
DT 06-A
8
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Gaps ö

2 TRIDEANQRATKMLGSG 18

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This sequence corresponds to residues 181-206 of the human 25 kD crynaptosomal associated protein (SNAP-25), and is a inhibitory agent of the invention. The agents of the invention inhibit secretion of the invention. The agents of the invention inhibit secretion of meuroransmitter from neuronal cells and is an excitation-secretory concupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally concrespond substantially to any one of AAW30099-W30102, or more generally concrespond substantially to any concentration of 10 microM, especially 0.25 microM, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit concrete spasticity. Also (I) may be absolided to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of imaging of intracellular distribution of substance p to brain tumourse for induction of apoptosis. Unlike the substance of the obtain tumourse for induction of apoptosis. Unlike the available. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required
                                Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Excitation-secretory uncoupling peptide(s) for inhibiting nuscle neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells.
Neurotransmitter secretion inhibitor #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 31; 61pp; English.
                                                                                                                                                                                                                                                                                                                                    96US-0013599P
                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-479986/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26 AA;
                                                                                                                                                                                                     WO9734620-A1.
                                                                                                                                                                                                                                                                                             18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                      18-MAR-1996;
                                                                                                                                                            Homo sapiens
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97WO-US004393.

ö Gaps ö y Match 100.0%; Score 84; DB 2; Length 26; Local Similarity 100.0%; Pred. No. 2.3e-07; hes 17; Conservative 0; Mismatches 0; Indels Query Match Matches ò

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AAE36682 standard; peptide; 33 AA. AAE36682;

07-AUG-2003 (first entry)

Goldfish SNAP-25A peptide

Goldfish, clostridium toxin; protease activity, botulinum toxin; BONT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; TeNT; cosmetic.

Goldfish; clostridium toxin; protease activity; botulinum toxin; BONT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

Carassius auratus

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulium serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance of spectrum overlapping the emission spectrum of the donor fluorophore and a ceptor and under the appropriate conditions, the resonance energy transfer is the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulium toxins of all serotypes and tetanus cotains (TeNT) in a sample including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast consertions are samples, cosmettics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, and to assay formulated clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is goldfish constitution.
                                                                                                                                                                                                                                                                                                                                                                                                         Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
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                                                               24. 25

10ce= "BONT/A sensitive cleavage site"

15. Note= "BONT/C sensitive cleavage site"
                               7. .8
/note= "BoNT/E sensitive cleavage site"
                                                                                                                                                                                                                                                                                                                                        Aoki KR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 42; 168pp; English
           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE36683 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                        Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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                                                                                                                                                                                                                                                                28-AUG-2001; 2001US-00942024.
                                                                                                                                                                                                                                 22-AUG-2002; 2002WO-US027145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TRIDEANQRATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 TRIDEANQRATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldfish SNAP-25B peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.7
Marches 17; Conservative
                                                                                                                                                                                                                                                                                                      (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-290198/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33 AA;
                                                                                                                                                         WO2003020948-A2
                  Key
Cleavage-site
                                                                     Cleavage-site
                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2003
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Mon Apr

TeNT; cosmetic

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a context and acceptor and under the appropriate conditions. The resonance energy transfer is call under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples. They are useful to assay a sample from a human or animal, for agamples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, and to assay formulated clostridial toxin and to assay formulated clostridial toxin products including pharmaceutics. The present sequence is goldfish SNAP-25B peptide used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                    Location/Qualifiers
7. .8
/note= "BONT/E sensitive cleavage site"
                                                                                                                 24. 25
/note= "BoNT/A sensitive cleavage site"
25. 26
                                                                                                                                                                              /note= "BoNT/C sensitive cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 100.0%; Pred. No. 3e-17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 42; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE36678 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TRIDEANORATKMLGSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002; 2002WO-US027145.
                                                                                                                                                                                                                                                                                                                              28-AUG-2001; 2001US-00942024
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                                                                                                                                                                                                                                                                                                                                                                (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-290198/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 17; Conserv
                                    Carassius auratus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNAP-25 peptide
                                                                                                                                                                                                                  WO2003020948-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33 AA;
                                                                                     Cleavage-site
                                                                                                                           Cleavage-Bite
                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                      Steward LE,
                                                                                                                                                                                                                                                      13-MAR-2003
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Aoki KR;

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BoNI/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a spectrum overlapping the emission spectrum of the donor fluorophore and a not complete the classification of the donor fluorophore and a complete the classification of the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulium toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast costed or proceased foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin and to assay formulated clostridial toxin and to assay formulated clostridial toxin and to assay formulated clostridial toxin and cosmetics. The present sequence is SNAP-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
               Human, clostridium toxin, protease activity, botulinum toxin, BoNT, TeNT,
tetanus toxin, VAMP, synaptobrevin, SNAP-25, syntaxin, pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                             24. .25
/note= "BoNT/A sensitive cleavage site"
                                                                                                                                                                                                                                                                                         25. .26
/note= "BONT/C sensitive cleavage site"
                                                                                                                                                                                                            7. .8
/note= "BoNT/E sensitive cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 3, 2006, 15:36:57 Job time: 97.607 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 42; 168pp; English.
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002; 2002WO-US027145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001US-00942024
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                                                         cosmetic; mouse; rat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-290198/28
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Best Local Similarity
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                                                                                                       Homo sapiens
                                                                                                                           Mus musculus
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                                                                                                                                                 Rattus sp.
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Matches
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Gaps ö

100.0%; Score 84; DB 6; Length 33; 100.0%; Pred. No. 3e-07; ive 0; Mismatches 0; Indels

us-09-942-098-93.rpr

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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3, 2006, 15:30:10 ; Search time 11.9083 Seconds (without alignments) 177.756 Million cell updates/sec April Run on:

US-09-942-098-93 99 Title: Perfect

1 XMEKTRIDEANQRATKMLGSGX 22 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		synapse protein sn	osomal-as		nerve terminal pro	synaptosomal-assoc	synapse protein -	synaptosomal-assoc	conserved hypothet	DNA-directed RNA p	=		٦,	-	lipoprotein [impor		homeobox protein (sorbitol dehydroge	hypothetical prote	outer membrane lip	hypothetical 13.9K	hypothetical prote	vesicle-membrane f	vesicle-membrane f	probable OmpA-fami	methyl-accepting c		serotonin receptor
ŒΙ	150481	I50480	A37861	I53735	167823	A33623	150552	A49708	D87525	A29959	JC5512	876238	T29999	T32127	G90551	AH3356	D96829	S71478	140014	T33167	A33854	G29826	AE1918	JC5297	JC5296	A10063	F96966	A33988	A53279
DB	7	N	~	~	~	N	~	7	7	~	7	N	N	~	7	7	N	~	~	7	~	~	7	7	7	N	7	7	7
% Query Match Length	203	204	206	206	206	206	210	29	296	1361	210	1578	2288	393	642	278	745	747	829	1056	83	125	139	158	211	536	575	1692	377
& Query Match	· o	o,	٥.	•	6.	89.9	64.6	51.5	49.5	48.0	46.5	46.5	46.5	45.5	45.5	44.4	44.4	44.4	44.4	42.9	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	41.9
Score	68	89	89	83	83	89	64	51	49	47.5	46	46	46	45	45	44	44	44	44	42.5	42	42	42	42	42	42	42	42	41.5
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MADS-box protein M ATP/GTP binding pr pre-mRNA enlicing	3 -		hypothetical prote hypothetical prote	probable NH(3)-dep lcrD protein – Yer	probable general s hypothetical prote	probable histidino	nibilathor denyaro hypothetical prote
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323	503 542	563 602	609 639	679 704	740	431	449 540
41.4	4 4 4 1 . 4 . 7 . 4 .	41.4	41.4	41.4	41.4	40.9	40.9
441	* 4 4 1 1 1	41 41	41	41	4 4 1	40.5	40.5
30	2 W W 2 W 4	32 36	37	39	4.1	43	4 4 5 4 5

ALIGNMENTS

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synapse protein SNAP-25 - goldfish (Cispecies: Carassius auratus (goldfish) (Cispecies: Carassius auratus (goldfish) (Cispecies: Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 (Cispecies: C.; Larhammar, D. (Cispecies: C.; Larhammar, D. (Cispecies: Date: Date: Data (Cispecies: Data) (Cispeci
RESULT 1
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Gaps ö Query Match

89.9%; Score 89; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels

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186 KTRIDEANQRATKMLGSG 203 4 KTRIDEANQRATKMLGSG 21

⋧ 셤 RESULT 2

C;Species: Carassius auratus (goldfish)
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50480
C;Accession: I50480
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish. A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50480
A;A

A;Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:g349426; PIDN:}C;Genetics: A;Gene: SNAP-25

ö Gape ö 89.9%; Score 89; DB 2; Length 204; ilarity 100.0%; Pred. No. 2.7e-07; Conservative 0; Mismatches 0; Indels Local Similarity les 18; Conserva Query Match Best Loca Matches

21 4 KTRIDEANQRATKMLGSG

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C;Accession: A49708
B;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; I)
J. Biol. T. (C.) 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Accession: A49708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; V
J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differer
A;Reference number: A33623; MUID:90078337; PMID:2592413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synapse protein - marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 15052
C;Accession: 15052
J. Blomgvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.J.
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shc.
A;Reference number: A49513; MUID:94043281; PMID:826991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UP10000135AFE; GB:L22020; NID:g431296; PIDN:J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A33623
A;Status: preliminary
A;Nolecule type: mRNA
A;Rolecule type: MRNA
A;Rolecule (A)
A;Rolecule (A)
A;Rolecule (A)
A;Rolecule (A)
A;Rolecule (A)
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:9200
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
                                                                                                                                                                      Gaps
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                                                                                                 Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Best Local Similarity 76.5%; Pred. No. 0.0043;
Matches 13; Conservative 1; Mismatches 3
                                                                                                 Query Match 89.9%; Score 89; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 18; Conservative 0; Mismatches
A, Cross-references: GDB:355671; OMIM:600322
A, Map position: 20p11.2-20p11.2
                                                                                                                                                                                                                                                                           189 KTRIDEANORATKMLGSG 206
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                                                                                                        synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicas, S.; Laxhammar, D.; Blomgvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C. Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid A;Reference number: A37861; MUID:91126080; PMID:1992470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nerve terminal protein - human
Cispecies: Homo sapiens (man)
Cjate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CjAccession: 153735
R;Bark, I.C.; Wilson, M.C.
Rene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: 153735; MUID:94156217; PMID:8112622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 167823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein A;Reference number: 153735; MUID:94156217; PMID:8112622
                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary
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A,Residues: 1-206 <CAT>
A,Cross-references: UNIPROT:P60878; UNIPARC:UPI000001103; GB:M57957; NID:g212673; PIDN:
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A;Molecule type: mRNA
A;Residues: 1-206 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:P60880; UNIPARC:UP1000002B3DD; GB:L19760; NID:g307425; PIDN
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Accession: IS3735 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

A; Residues: 1-206 < RES>

189 KTRIDEANQRATKMLGSG 206

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A;Cross-references: GDB:355671; OMIM:600322 A;Map position: 20p11.2-20p11.2

A; Gene: GDB: SNAP

189 KTRIDEANQRATKMLGSG 206

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RESULT 5

Genetics: Gene: GDB:SNAP

4 KTRIDEANQRATKMLGSG 21

Query Match Best Local Similarity 100.0 Matches 18; Conservative

Gaps

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CySpecies: Mus musculus (house mouse)
CySpecies: Mus musculus (house mouse)
CyDate: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
CyAccession: JC5512
Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Okaz Bychem. Biophys. Res. Commun. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Muncl8c.
A;Reference number: JC5512; MUID:97312558; PMID:9168999
A;Molowil CySS12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: X
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Synechocystis sp.
A; Variety: PCC 6803
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: St. PCC 6803
C; Spaces: St. PCC 6803
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1578 <KAN>
A;Cross-references: UNIRROT:P74400; UNIPARC:UPI00000C10E9; EMBL:D90914; GB:AB001339; NID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1.210 *ARA>
A,Crose-references: UNIPROT:009044; UNIPARC:UPI0000022BSC; DDBJ:AB000822; NID:g2189950; I
A,Croment: This protein is involved in the insulin-induced translocation of vesicles cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-2288 <LAT>
A;Cross-references: UNIPROT:Q23081; UNIPARC:UPI000017BCB7; EMBL:U64862; PIDN:AAB52624.1;
A;Experimental source: strain Bristol N2; clone ZC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZC8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein sll0267 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2; Length 1578;
Pred. No. 39;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S76238
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T29999 R.;Accession: T29999 R;Latreille, P.; Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
submitted to the EMBL Data Library, July 1996
A;Reference number: Z20719
A;Reference number: Z20719
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule rype: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2;
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 LDAIQLDQANQRAQNQLG 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 KNRIDIANTRAKKLIDS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KTRIDEANORATKMLGS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 44.4%; les 8; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.5%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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C;Accession: D87525
B; i.e., Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter creacentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hudson, G.S.; Holton, T.A.; Whitfeld, P.R.; Bottomley, W. J. Mol. Biol. 200, 639-654, 1988
A;Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA A;Reference number: A29959; MUID:88316931; PMID:3045324
A;Accession: A29959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1361 <HUD>
A;Cross-references: UNIPROT:P11704; UNIPARC:UP10000134774; EMBL:M55297; NID:g295119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein CC2229 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr.2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                           Query Match 51.5%; Score 51; DB 2; Length 29; Best Local Similarity 65.0%; Pred. No. 0.074; Matches 13; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
49.5%; Score 49; DB 2;
Best Local Similarity 55.6%; Pred. No. 2;
Matches 10; Conservative 2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47.5; DB; Pred. No. 19; 4; Mismatches
                                                                                                                                          A, Cross-references: UNIPARC: UPI000017C9D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| ||| |:| |:|||
LEK-RIDSWNERITRILGS 1170
                                                                                                                                                                                                                                                                                                                                                           12 MEKA--DSNKTRATKMLGSG 29
                                                                                                                                                                                                                                                                                                                   2 MEKTRIDEANORATKMLGSG 21
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nes 11; Conservative
                                                                           A;Molecule type: protein A;Residues: 1-29 <BIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-296 <STO>
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                                                      preliminary
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A;Gene: CC2229
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Gaps

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RESULT 11

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lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Accession: G90551
Nucleic Acids Res. 29, 2145-2153, 2001
Nucleic Acids Res. 29, 2145-2153, 2001
Nyritle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUD:21267165; PMID:11353084
A;Accession: G90551
A;Accession: G90551
A;Residual ary
A;Molecule type: DNA
A;Residuals: 1-642 cKUR>
A;Residuals: 1-642 cKUR>
A;Cross-references: UNIPROT: Q980P2; UNIPARC: UPI00000C8060; GB:AL445566; PID:g14089733; E
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-39 < clam.
A;Residues: 1-39 < clam.
A;Cross-references: UMIPROT:O16766; UNIPARC:UPI00001642E9; EMBL:AF016686; PIDN:AAB66239.
A;Experimental source: strain Bristol N2; clone R07C3
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                                                                                                                                                                                                                                                                                                                      hypothetical protein R07C3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32127
R;Lamar, B.; Kramer, J.
R;Lamar, B.; Kramer, J.
R;Description: The sequence of C. elegans cosmid R07C3.
A;Reference number: Z21127
A;Reference number: Z21127
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A,Map position: 2
A,Introns: 20/1; 350/2
C,Superfamily: Caenorhabditis elegans hypothetical protein C32B5.10
Query Match
46.5%; Score 46; DB 2; Length 2288;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 9; Conservative 2; Mismatches 4; Indels
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Best Local Similarity 44.4%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.5%; Score 45; DB 2; Length 393; Best Local Similarity 60.0%; Pred. No. 13; Matches 9; Conservative 2; Mismatches 4; Indels
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                                                                                                                                                                                    626 KTRIDELNRRVENLL 640
                                                                                                                         4 KTRIDEANORATKML 18
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A;Genetic code: SGC3
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Goldfish Goldfish Synaptoso

Mouse syn Mouse SNA

Aab15584 Aab13169 Aac15002 Aac15165 Abw017104 Abw017104 Aaw301001 Aaw301001 Aaw791001 Aaw79109 Aaw79198 Aau00253 Aau00253 Aau00253 Aau00252 Aau00252 Aau00253 Aae36667 Aae36667 Aae36667 Aae36667

Clostridi Clostridi Murine SN Goldfish

Synaptoso SNARE hom SNARE hom

SNARE hom Human SNA

VAMP-

Rat Prote Rat Prote Rat Prote

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

Result No.

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Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 93 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium toxin; protease activity; botulinum toxin; BONT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fret substrate peptide #9 used in the invention.
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AAO15165
AAO1104
ABW01715
ADW97001
AEA14904
ARA130103
AAW43426
AAW43426
AAW730246
AAW70253
AAW7366253
AAW7366253
AAW70246
AAW7366253
                                                   AAB15584
ADP13169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE36738 standard; peptide; 22 AA.
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(ALLR ) ALLERGAN INC
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Goldfish
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Goldfish
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Goldfish
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                                                                                                                                                                                        ; Search time 112.826 Seconds (without alignments) 85.675 Million cell updates/sec
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Aae36737 F
Aae36737 F
Abw01793 F
Abw01796 F
Abw01796 F
Aae36733 E
Abw01791 F
Abw01794 F
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                                   GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
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                                                                                                                                          protein search, using sw model
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AAE36733
ABW01789
AAE36735
ABW01791
AAE36682
AAE36682
AAE36678
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ABW01793
ABW01796
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                                                                                                                                                                                                                                                                                                                                                      1 XMEKTRIDEANQRATKMLGSGX
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geneseqp2003bs:*
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Maximum Match 100%
Listing first 45 sv
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.: geneseqp1980s:*
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geneseqp20028:*
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geneseqp2005s:*
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Maximum DB seq length: 200000000
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99
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Match Length
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The present invention relates to novel clostridium toxin substrates invention further relates to botulinum serotype A/E (BONT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance appetrum overlapping the emission spectrum of the donor fluorophore and about A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the procease activity of any clostridial toxin including bactulinum toxins of all serotypes and tetamus toxins (TeNT) in a sample including bacterial, baculoviral and yeast the procease of the invention of all serotypes and tetamus and the contraction of the invention of all serotypes and procease and tetamus and the contraction of the invention of all serotypes and procease and tetamus and the contraction of the invention of all serotypes and procease and the contraction of the invention of all serotypes and procease and tetamus and the contraction of the invention of the invention of the procease and tetamus and the contraction of the contraction of the invention of the contraction of the contractio
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Gaps ö 100.0%; Score 99; DB 6; Length 22; 100.0%; Pred. No. 3.8e-09; 0; Indels 0; Mismatches 2 MEKTRIDEANORATKMLGSG 21 20; Conservative Local Similarity Query Match Best Loca Matches 윤 ð

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Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer. FRET substrate #7 to analyse proteolytic activity of botulinum toxin. ABW01794 standard; peptide; 22 AA (first entry) Modified-site Modified-site Unidentified 12-FEB-2004 ABW01794; ABW01794 THE CONTRACTOR OF THE PROPERTY OF THE PROPERTY

/note= "Tetramethylrhodamine labelled lysine; C-terminal /note= "Fluoresceinated lysine' Location/Qualifiers amide"

US2003143651-A1

31-JUL-2003

28-AUG-2001; 2001US-00942098

28-AUG-2001; 2001US-00942098

œ. FERNANDEZ-SALAS (STEW/) STEWARD L E.

Aoki KR; Steward LE, Fernandez-Salas E,

AOKI K R.

(AOKI/)

WPI; 2003-829791/77.

Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.

The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BONT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor

Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.

WPI; 2003-290198/28.

Example 1; Page 115; 168pp; English.

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                              The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "EDANS-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 95 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                Gaps
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                                                                                                                                                   100.0%; Score 99; DB 7; Length 22; 100.0%; Pred. No. 3.8e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Fret substrate peptide #11 used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                     AAE36740 standard; peptide; 19 AA.
            Example 1; Page 29; Opp; English.
                                                                                                                                                                                                           2 MEKTRIDEANORATKMLGSG 21
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Matches 20; Conservative
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                                                                                                                               Sequence 22 AA;
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Modified-site
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and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP. (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 92 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium toxin; protease activity; botulinum toxin; BONT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                   Length 19;
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                                                                                                                                                                                                                                                                                   89.9%; Score 89; DB 100.0%; Pred. No. 1.5 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                      specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2002; 2002WO-US027145
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Les 18; Conservative
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                                                                                                                                                                                                                                                        Sequence 19 AA;
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Modified-site
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Matches
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Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.

Example 1; Page 115; 168pp; English

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Gaps

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BONT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a ceptor shown as a paraparate conditions. The resonance energy transfer is the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium curing the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus contributed toxin including botulinum toxins of all serotypes and tetanus contributed including botulinum toxins of all serotypes and tetanus contributed toxin including botulinum toxins of all serotypes and tetanus contributed amples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for camples. They are useful to assay a sample from a human or animal, for contridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret including pharmaceuticals and cosmetics. The present sequence is fret.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Tetramethylrhodamine labelled lysine; C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRET substrate #6 to analyse proteolytic activity of botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                          89.9%; Score 89; DB 6; Length 19; 100.0%; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABW01793 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PTTTPEANGRATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KTRIDEANQRATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEW/) STEWARD L E. (FERN/) FERNANDEZ-SALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-829791/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps

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Score 89; DB 7; Length 19; Pred. No. 1.5e-07; 0; Mismatches 0; Indels

89.>\, 100.0\; PE\

18; Conservative

Query Match Best Local Similarity Matches 18; Conserv

89.68;

1 KTRIDEANQRATKMLGSG 18

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4 KTRIDEANQRATKMLGSG

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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                             assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRET substrate #9 to analyse proteolytic activity of botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "EDANS labelled lysine; C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 19;
1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRET; flourescence resonance energy transfer
                                                                                                                                                                                                                                                                                                                                                 89.9%; Score 89; DB 100.0%; Pred. No. 1.5 ive 0; Mismatches
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                           Opp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABW01796 standard; peptide; 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KTRIDEANORATKMLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LACAV) FERNANDEZ-SALAS E. (AOKI/) AOKI K R. STEWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
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                           Example 1; Page 29;
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                Sequence 19 AA;
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ABW01796
ABW
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Sequence 19 AA;

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This sequence corresponds to residues 187-206 of the human 25 kD synaptosomal associated protein (SNAP-25), and is a inhibitory agent of the invention. The agents of the invention inhibit secretion of meurotransmitter from neuronal cells and is an excitation-secretory uncoupling peptide (I) of at least 20 anino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally correspond substantially to any one of AAW30097-W30102, or more generally correspond substantially to any one of AAW30097-W30102, or more generally correspond finhibits 50% of catecholamine secretion from bowine chromaffin cells at a concentration of 10 microW, especially 0.25 microW, or lease of neurotransmitters from synaptic vesicles, specifically for reducing muscle spaticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of the drug to neural cells provide targeted drug delivery, e.g. of the control of 10 are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required
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                                                                                                                                                                         Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Excitation-secretory uncoupling peptide(s) for inhibiting nuscle neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells.
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Pred. No. 1.6e-07;
0; Mismatches 0;
                                                                                                                                              Neurotransmitter secretion inhibitor #4.
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100.0%; Pre
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                                  AAW30100 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                         06-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-479986/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1997;
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                WO9734620-A1
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                                                                                                                                                                                                                                                                                                                                                      25-SEP-1997
                                                                         AAW30100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montal M;
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Matches
RESULT 7
                   AAW30100
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Best Local Similarity

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BoNT/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and acceptor spectrum overlapping the emission spectrum of the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium convincions are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus conting (TeNT) in a sample including botulinum toxins of all serotypes and tetanus lysate, raw, cooked or processed foods, beverages, animal feed, soil samples. They are useful to assay a sample from a human or animal, for egg, exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin, products assay formulated clostrin products
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 88 in the sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention
                                                                                                                                                                                     Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                           /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 88 ithe sequence listing of the specification"
                                                                                                                                                  Fret substrate peptide #4 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 115; 168pp; English
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                  AAE36733 standard; peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002; 2002WO-US027145.
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                                                                                                                                                                                                                                                                                                                 Key
Modified-site
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                                                                                                                                                                                                                                                                        Inidentified
                                                                                                               07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2003
                                                                           AAE36733;
                                                                                                                                                                                                                                     cosmetic.
RESULT 8
                    AAE36733
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Aoki KR;

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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                            "Tetramethylrhodamine labelled lysine; C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assaying for the procease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence toxins of all serotypes as well as tetanus toxins. The present sequence tis FRET (flourescence resonance encoy, ransfer) substrate to analyse proceolytic activity of botulinum toxin. This substrate is used in the
                                                                                                                                                                                                                                                   Clostridial toxin; protease activity; tetanus toxin; botulinum toxin; FRET; flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                   Gaps
                                                                                                                                                                                                                           FRET substrate #2 to analyse proteolytic activity of botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides clostridial toxin substrates useful
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                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 89; DB 7; Le
100.0%; Pred. No. 1.8e-07;
ive 0; Mismatches 0;
       Pred. No. 1.8e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    'note= "Fluoresceinated lysine"
                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aoki KR
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                               ABW01789 standard; peptide; 23 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteolytic activity of botulinum exemplification of the invention
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steward LE, Fernandez-Salas E,
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                                                                  5 KTRIDEANQRATKMLGSG
                                                 4 KTRIDEANQRATKMLGSG
                                                                                                                                                                                                   (first entry)
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18; Conservative
                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEWARD L E.
FERNANDEZ-SALAS
                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-829791/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AOKI/) AOKI K R.
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                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                    12-FEB-2004
                                                                                                                                                                                                                                                                                                  Inidentified
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AAE36735
ID AAE36
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                        Matches
                                                                                                                    RESULT 9
ABW01789
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6 KTRIDEANQRATKMLGSG 23

(first entry)

Location/Qualifiers

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invention further relates to botulinum serotype A/E (BONN/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BONT A or BONN/E recognition sequence comprising a cleavage site, where the cleavage site intervens between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including bacterial, baculoviral and yeast toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples. They are useful to assay a samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret unbatrate peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to novel clostridium toxin substrates. The
                                                                                                                              Clostridium toxin, protease activity, botulinum toxin, BONT, TeNT, tetanus toxin, VAMP, synaptobrevin; SNAP-25, syntaxin, pharmaceutical,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 89.9%; Score 89; DB 6; Le Local Similarity 100.0%; Pred. No. 1.9e-07; les 18; Conservative 0; Mismatches 0;
                                                                                             Fret substrate peptide #6 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 115; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2002; 2002WO-US027145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001US-00942024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPI; 2003-290198/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003020948-A2
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                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                  Unidentified
                                                         07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steward LE,
                                                                                                                                                                           cosmetic.
                  AAE36735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Aoki KR;

Fernandez-Salas E,

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Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
                                                                                                                                                                                                                                                                                           /note= "Tetramethylrhodamine labelled lysine; C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (flourescence resonance energy transfer) substrate to analyse proteclytic activity of botulinum toxin. This substrate is used in the
                                                                                                                                                    Clostridial toxin, protease activity, tetanus toxin, botulinum toxin, FRET, flourescence resonance energy transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                       FRET substrate #4 to analyse proteolytic activity of botulinum toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.9%; Score 89; DB 7; Length 24; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                              /note= "Fluoresceinated lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aoki KR
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30099 standard; peptide; 26 AA.
                              ABW01791 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 29; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001US-00942098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KTRIDEANQRATKMLGSG
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STEW/) STEWARD L E. (FERN/) FERNANDEZ-SALAS
                                                                                                                                                                                                                                                                                                                amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-829791/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AOKI/) AOKI K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 AA;
                                                                                                                                                                                                                                                                                                                                           US2003143651-A1
                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                     Unidentified
                                                                                          12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2003.
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                                                             ABW01791;
RESULT 11
ABW01791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW30099
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                                           SAXXXX
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                                                                                                                                                                                                                                               /note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 90 in the sequence listing of the specification"
                                                                                                                                                                                   /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 90 in the sequence listing of the specification"
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Gaps

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4 KTRIDEANQRATKMLGSG 21

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Best Loc Matches

Length 24; Indels

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This sequence corresponds to residues 181-206 of the human 25 kD synaptosomal associated protein (SNAP-25), and is a inhibitory agent of the invention. The agents of the invention inhibit secretion of the invention. The agents of the invention inhibit secretion of correspond substantially to any one of AAM30097-W30102, or more generally correspond substantially to any one of AAM30097-W30102, or more generally correspond substantially to any one of AAM30097-W30102, or more generally correspond substantially to any one of AAM30097-W30102, or more generally correspond substantially to any one of AAM30097-W30102, or more generally correspond substantially to any one of AAM30097-W30102, or more generally correspond substantially as a replacement for Clostridium toxin, to inhibit correction muscle spacificity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of substance P to brain tumours for induction of apoptoals Unite the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required
                                Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells.
Neurotransmitter secretion inhibitor #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 31; 61pp; English.
                                                                                                                                                                                                                                                                                           97WO-US004393
                                                                                                                                                                                                                                                                                                                                     96US-0013599P
                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-479986/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 AA;
                                                                                                                                                                                                                                                                                           18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                       18-MAR-1996;
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                     MO9734620-A1
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           Gaps
Length 26;
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ö 0; Indels 89.9%; Score 89; DB 2; Le 100.0%; Pred. No. 2.1e-07; ive 0; Mismatches 0; 21 4 KTRIDEANQRATKMLGSG 18; Conservative Query Match Best Local Similarity Matches Š

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9 KTRIDEANQRATKMLGSG

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AAE36682 standard; peptide; 33 AA. 07-AUG-2003 (first entry) Goldfish SNAP-25A peptide AAE36682; AAE36682 SXXXXXXXXXXXXXXXX

Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; TeNT; cosmetic.

Carassius auratus.

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The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BONT/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a spectrum overlapping the emission spectrum of the donor fluorophore and a contract and under the appropriate conditions, the resonance energy transfer is cand under the appropriate conditions, the resonance energy transfer is cand under the appropriate conditions, the resonance energy transfer is cand under the appropriate conditions, the protesse of clostridium control invention are useful in assaying for the protesse activity of any clostridial toxin including botulium toxins of all serotypes and tetanus control in a sample including bacterial baculoviral and yeast toxins (TeNT) in a sample including bacterial baculoviral and yeast control samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for samples. They are useful to assay a sample from a human or animal, for callostridial toxin, to follow activity during production and purification of clostridial toxin and cosmetics. The present sequence is goldfish
                                                                                                                                                                                                                                                                                                                                                                                                   Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                   25. .26
/note= "BoNT/C sensitive cleavage site"
                                   '. .8
'note= "BoNT/E sensitive cleavage site"
                                                                                   "BoNT/A sensitive cleavage site"
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100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                    Aoki KR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNAP-25A peptide used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 42; 168pp; English
                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE36683 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                    Steward LE, Fernandez-Salas E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                               22-AUG-2002; 2002WO-US027145
                                                                                                                                                                                                                                                                  28-AUG-2001; 2001US-00942024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goldfish SNAP-25B peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                    24. .25
/note= "l
                                                                                                                                                                                                                                                                                                   (ALLR ) ALLERGAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-290198/28
                                                                                                                                                            WO2003020948-A2
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                                   Cleavage-site
                                                                      Cleavage-site
                                                                                                         Cleavage-site
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                                                                                                                                                                                               13-MAR-2003.
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    24. .25
    /note= "BoNT/A sensitive cleavage site"
    25. .26

                          7. .8
/note= "BoNT/E sensitive cleavage site"
                                                     /note= "BoNT/C sensitive cleavage site"
                   Location/Qualifiers
                                                                                                                       Fernandez-Salas E,
                                                                                       22-AUG-2002; 2002WO-US027145.
                                                                                                  28-AUG-2001; 2001US-00942024
                                                                                                            (ALLR ) ALLERGAN INC
                                                                                                                                  WPI; 2003-290198/28.
          Carassius auratus
                                                                 WO2003020948-A2
                                                                                                                                                                                                                                                                                                  Sequence 33 AA;
TeNT; cosmetic.
                                      Cleavage-site
                          Cleavage-site
                                                Cleavage-site
                                                                                                                       Steward LE,
                                                                            13-MAR-2003
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ö Gaps ö 89.9%; Score 89; DB 6; Length 33; 100.0%; Pred. No. 2.7e-07; 0; Indels 100.0%; Prea. 18; Conservative Query Match Best Local Similarity Matches 18; Conserv

33

07-AUG-2003 (first entry) SXAXAXB

RESULT 15 AAE36678 SNAP-25 peptide

The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/B (BoWT/A/B) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and about A or BoNT/E recognition spectrum of the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including boculinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast layere, and processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is goldfish SNAP-25B peptide used in the invention Botulinum serotype A/B substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site. Disclosure; Page 42; 168pp; English

2 4 KTRIDEANQRATKMLGSG

d AAE36678 standard; peptide; 33 AA.

Human, clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; cosmetic; mouse; rat.

Homo sapiens

musculus Rattus sp

7. .8 'note= "BoNT/E sensitive cleavage site" 'note= "BoNT/A sensitive cleavage site" 24. .25 Cleavage-site Cleavage-site

Location/Qualifiers

25. 26 /note= "BONT/C sensitive cleavage site" Cleavage-site

WO2003020948-A2

13-MAR-2003.

22-AUG-2002; 2002WO-US027145.

Aoki KR;

28-AUG-2001; 2001US-00942024

(ALLR) ALLERGAN INC

Aoki KR; Steward LE, Fernandez-Salas E,

WPI; 2003-290198/28

Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.

Disclosure; Page 42; 168pp; English.

The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a prectrum overlapping the emission sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulium toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast colstridial toxin including bacterial, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having production and purification of clostridial toxin and to assay formulated clostridial toxin and cosmetics. The present sequence is SNAP-25 including pharmaceutics. The present sequence is SNAP-25 peptide used in the invention

Sequence 33 AA;

Gaps ö Score 89; DB 6; Length 33; Pred. No. 2.7e-07; Indels ö Mismatches 89.9%; Scu. 100.0%; Pre Local Similarity 100. Query Match Best Loca Matches

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3, 2006, 15:36:56 Search completed: April Job time: 113.992 secs

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57.210 Million cell updates/sec
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Sequence 33,
Sequence 35,
Sequence 35,
Sequence 1, A
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Sequence 40,
Sequence 41,
Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 4, Sequence 1, Sequence 1, Sequence 2, Sequence 2, Sequence 2, Sequence 22, Sequence 20, Sequence 20, Sequence 12, Sequence 12
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                                                                                                                                                                                                                                                   April 3, 2006, 15:49:32 ; Search time 11.7064 Seconds
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2: /SIDSS/ptcdata/1/pubpaa/US07_NEW_FUB.pep:*

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4: /SIDSS/ptcdata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDSS/ptcdata/1/pubpaa/US09_NEW_FUB.pep:*

7: /SIDSS/ptcdata/1/pubpaa/US10_NEW_FUB.pep:*

8: /SIDSS/ptcdata/1/pubpaa/US11_NEW_FUB.pep:*

8: /SIDSS/ptcdata/1/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-948-097-36

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US-10-948-097-41

US-10-947-071-4

US-10-948-097-1

US-10-948-097-2

US-10-948-097-2

US-10-948-097-2

US-10-948-097-2

US-10-948-097-20

US-10-948-097-30

US-10-948-097-33

US-10-948-097-33

US-10-948-097-33

US-10-948-097-33

US-10-948-097-33

US-10-948-097-33

US-10-948-097-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-947-071-36
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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	US-10-980-346B-38	9	11	67.7	63	44	
62,	US-10-948-097-62	9	11	68.7	68	43	
58,	US-10-948-097-58	9	17	68.7	68	42	
54,	US-10-948-097-54		17	68.7	68	. 41	
62,	US-10-947-071-62		17	68.7	68	40	
58,	US-10-947-071-58		11	68.7	68	39	
4.	US-10-947-071-54		17	68.7	68	38	
	US-10-948-097-60		11	69.7	69	37	
22,	US-10-948-097-55		17	69.7	69	36	
23	US-10-948-097-53		17	69.7	69	35	
34,	US-10-948-097-34	9	17	69.7	69	34	
9	US-10-947-071-60		17	69.7	69	33	
	US-10-947-071-55		17	69.7	69	32	
23,	US-10-947-071-53		17	69.7	69	31	
34,	US-10-947-071-34		17	69.7	69	30	
	US-10-948-097-32	9	16	69.7	69	29	
32,	US-10-947-071-32	9	16	69.7	69	28	
61,	US-10-948-097-61	9	11	70.7	70	27	
	US-10-947-071-61	9	11	7.07	70	26	

ALIGNMENTS

Gaps

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Sequence 40, Application US/10948097

Sequence 40, Application US/10948097

Publication No. US2006006322A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

APPLICANT: Steward, Lance

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REPERENCE: 66872-440

CURRENT APPLICATION NUMBER: US/10/948,097

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 33
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US-10-948-097-41

Sequence 41, Application US/10348097

Publication No. US20060063222A1

Publication No. US2006006322A1

GENERAL INFORMATION:

APPLICANT: Williams, Dudley J.

APPLICANT: Steward, Lance

APPLICANT: Acin Kei Reger

TITLE OF INVENTION: Fluorescence Polarization Assays For

TITLE OF INVENTION: Pluorescence Polarization Assays For

TITLE OF INVENTION: Determining Clostridial Toxin Activity

FILE REFERENCE: 66872-040

CURRENT PAPLICATION NUMBER: US/10/948,097

CURRENT PILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 4: GEG ID NOS: 96

SEG ID NO 4: GEG ID NO 5: GEG I
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   Indels
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100.0%; Pred. No. 5.1e-09;
tive 0; Mismatches 0;
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                                                                     4 KTRIDEANORATKMLGSG 21
                                                                                                                             16 KTRIDEANORATKWLGSG 33
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Matches 18; Conservative
18; Conservative
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US-10-948-097-40
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US-11-195-098-11
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LENGTH: 33
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| Sequence 41. Application US/10947071
| Sequence 41. Application No. US2066063221A1
| Publication No. US2066063221A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Dudley J.
| APPLICANT: Gimore, Marcella
| APPLICANT: Steward, Lance
| APPLICANT: Aoki, Kei Roger
| TITLE OF INVENTION: For Determining Clostridial Toxin Activity
| FILE REFERENCE: 66872-043
| CURRENT APPLICANTON NUMBER: US/10/947,071
| CURRENT PILING DATE: 2004-09-21
| NUMBER OF SEQ ID NOS: 101
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 41
| LENGTH: 33
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Sequence 36, Application US/10948097

Sequence 36, Application US/10948097

Sequence 36, Application US/10948097

Sequence 36, Application US/10948097

Sequence 36, Marcella APPLICANT: Verhagen, Marcella APPLICANT: Glimore Marcella APPLICANT: Steward, Lance

CURRENT FILE OF INVENTION: Determining Clostridial Toxin Activity

FILE REFRENCE: 66872-040

CURRENT FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36

LENGTH: 33

TYPE: PRT

TYPE: PRT

CURRANISM: Mus musculus

US-10-948-097-36
                                                                                                                                                                                                                                          Query Match 89.9%; Score 89; DB 6; Length 33; Best Local Similarity 100.0%; Pred. No. 5.1e-09; Matches 18; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 5.1e-09;
tes 18; Conservative 0; Mismatches 0;
   SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                 TYPE: PRT; ORGANISM: Carassius auratus
US-10-947-071-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Carassius auratus
US-10-947-071-41
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Best Local Similarity
                               SEQ ID NO 40
LENGTH: 33
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Matches
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; Sequence 1, Application US/10947071
; Publication No. US2060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Verhagen, Marc
; APPLICANT: Verhagen, Marc
; APPLICANT: OF INVENTION: Lanchanide-Based Substrates and Methods
; TITLE OF INVENTION: Por Determining Clostridial Toxin Activity
; FILE REPRENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
: LENGTH: 206
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Sequence 4, Application US/10948097;
Publication No. US20060063222A1
GENERAL INFORMATION:
APPLICANT: Verhagen, Marc
APPLICANT: Williams, Dudley J.
APPLICANT: Glamore, Marcella
APPLICANT: Glamore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Aoki, Kei Roger
ITILE OF INVENTION: Determining Clostridial Toxin Activity
FILE REFERENCE: 66872-040
CURRENT APPLICANTON NUMBER: US/10/948,097
CURRENT APPLICANTON NUMBER: US/10/948,097
CURRENT APPLICANTON WINGER: 904-09-22
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 203
TYPE: PRT
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89.9%; Score 89; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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APPLICANT: Gilmore, Marcella
APPLICANT: Steward, Lance
APPLICANT: Verhagen, Marc
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 203;
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Publication No. US20060063221A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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CRGANISM: Homo sapiens
US-10-947-071-1
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US-10-947-071-1
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           Sequence 11, Application US/11195098

Publication No. US20050287622A1

GENERAL INFORMATION

APPLICANT: Schmidt, James J.

APPLICANT: Schmidt, James J.

APPLICANT: Schmidt, James J.

TITLE OF INVENTION: High Throughput Assays for the Protecolytic Activities of Clostrid

TITLE OF INVENTION: Neurotoxins

TITLE OF INVENTION: Neurotoxins

TITLE OF INVENTION: NUMBER: US/11/195,098

CURRENT APPLICATION NUMBER: US/10/802,574

PRIOR APPLICATION NUMBER: US/0962,360

PRIOR PILING DATE: 2004-03-17

PRIOR APPLICATION NUMBER: US 60/235,050

PRIOR APPLICATION NUMBER: US 60/235,050

PRIOR PILING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 11

LEASTH: 116

LEASTH: 116

LEASTH: 116
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; Sequence 4, Application US/100947071
; Publication No. US20060063221A1
; Publication No. US20060063221A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Dudley J.
    APPLICANT: Steward, Lance
    APPLICANT: Verhagen, Marcella
    APPLICANT: Verhagen, Marcella
    APPLICANT: Verhagen, Marcella
    APPLICANT: OF INVENTION: Lanthanide-Based Substrates and Methods
    TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
    TITLE OF INVENTION: For Determining Clostridial Toxin Activity
    FILE REPRENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT PILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOPTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
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89.9%; Score 89; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.9%; Score 89; DB 7; Length 116; Best Local Similarity 100.0%; Pred. No. 2.2e-08; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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US-10-948-097-4
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us-09-942-098-93.rapbn

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Gaps

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Length 206;

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Query Match

89.9%; Score 89; DB
Best Local Similarity 100.0%; Pred. No. 4.4
Matches 18; Conservative 0; Mismatches
           ORGANISM: Mus musculus
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US-10-947-071-20
                                 US-10-948-097-2
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US-10-946-097-1
i Sequence 1, Application US/10948097
i Publication No. US20060063222A1
i GENERAL INFORMATION:
i APPLICANT: Verhagen, Marcella
i APPLICANT: Gilmore, Marcella
i APPLICANT: Gilmore, Marcella
i APPLICANT: Braward, Lance
i APPLICANT: Brook, Kei Rook, Roo
TITLE OF INVENTION: For Determining Clostridial Toxin Activity FILE REPERBYCE: 66872-043
CURRENT APPLICATION NUMBER: US/10/947,071
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 101
SSGTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 206
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Sequence 2, Application US/10948097;
Publication No. US2006006322241
GENERAL INFORMATION:
APPLICANT: Williams, Dudley J.
APPLICANT: Williams, Dudley J.
APPLICANT: Steward, Lance, Marcella
APPLICANT: Steward, Lance
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100.0%; Pred. No. 4.4
:ive 0; Mismatches
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Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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LENGTH: 206
TYPE: PRT
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Sequence 225, Application US/11169041

Publication No. US20060019284A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: LOMPOINDS TRAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: COMPOUNDS TRAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT PELING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR PILING DATE: 2004-06-30
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; Sequence 20, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
    APPLICAMT: Walliams, Dudley J.
    APPLICAMT: Gilmore, Marcella
    APPLICAMT: Steward, Lance
    APPLICAMT: Verhagen, Marc
    APPLICAMT: Application: For Determining Clostridial Toxin Activity
    TITLE OF INVENTION: Earthanide-Based Substrates and Methods
    TITLE OF INVENTION: Lanchanide-Based Substrates and Methods
    TITLE OF INVENTION: Earthanide-Based Substrates
    TITLE OF INVENTION: For Determining Clostridial Toxin Activity
    TITLE OF INVENTION UNMERS: US/10/947,071
    CURRENT APPLICATION NUMBER: US/10/947,071
    CURRENT FILING DATE: 2004-09-21
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 20
    LENGTH: 334
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Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Plasmid pQBI GFP-SNAP25
US-10-947-071-20
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SOFTWARE: Patentin version 3.2
SEQ ID NO 225
LENGTH: 206
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ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-11-169-041-225
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Search completed: April 3, 2006, 15:58:09 Job time : 11.7064 secs

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1223, Ap 2, Appli 12, Appl 90, Appl 86, Appl 88, Appl 92, Appl 95, Appl

Title: Perfect score:

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100.0%; Score 99; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 93, Application US/09942024
; Sequence 93, Application No. US20030143650A1
; Bublication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Fortandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93

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Sequence 93, Application US/09942098
Sequence 93, Application No. US20030143651A1
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Pernandea-Salas, Ester
APPLICANT: APPLI
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NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa=fluorescein-modified lysine
US-09-942-024-7
US-09-942-024-12
US-09-942-098-2
US-09-942-098-2
US-10-261-161-4
US-10-261-161-4
US-10-261-161-4
US-10-261-161-109
US-10-261-161-109
US-10-273-860-1223
US-10-917-844-12
US-10-917-844-90
US-10-917-844-92
US-10-917-844-92
US-10-917-844-92
US-09-942-024-92
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| LOCATION: (0) ...(0)
| OTHER INFORMATION: at the C-terminal
US-09-942-024-93
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ORGANISM: Artificial Sequence
        NAME/KEY: MOD_RES
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             FEATURE:
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                                                                                                                                                                                                   April 3, 2006, 15:46:49; Search time 94.6606 Seconds (without alignments) 97.107 Million cell updates/sec
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Sequence 3
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1: /cgn2_6/ptodata/1/pubpāa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

1: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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OTHER INFORMATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 22
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa=fluorescein-modified lysine NAME/KEX: MOD_RES LOCATION: 20 OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine NAME/KEX: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 99; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 88, Application US/09942024

Sequence 88, Application No. US2003014365041

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: APPLICANTOR: Fer Protease Assays For Botulinum
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT PAPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 23
LENGTH: 23
TYPE: RRT
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                           PEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEX: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: at the C-terminal US-09-942-024-88
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OTHER INFORMATION: at the C-terminal
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NAME/KEY: MOD_RES
LOCATION: 1
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KTRIDEANORATKMLGSG 22

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine NAME/KEY: AMIDATION
Sequence 88, Application US/09942098
| Publication No. US20030143651A1 |
| GENERAL INFORMATION |
| APPLICANT: Steward |
| APPLICANT: Steward |
| APPLICANT: Steward |
| TITLE OF INVENTION: Fret Protease Assays For Clostridial |
| TITLE OF INVENTION: Toxins |
| FILE REFERENCE: P-AR 4802 |
| CURRENT APPLICATION UNMER: US/09/942,098 |
| CURRENT FILING DATE: 2001-08-28 |
| NUMBER OF SEQ ID NOS: 96 |
| SEQ ID NO 8 |
| SEQ ID NO 8 |
| LENGTH: 23
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89.9%; Score 89; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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Sequence 90, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas,
TITLE OF INVENTION: Free Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803

CURRENT APPLICANTON NUMBER: US/09/942,024

CURRENT PILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 90

LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
LOCATION: Xaa=fluorescein-modified lysine
NAME/KEY: MOD_RES
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INFORMATION: at the C-terminal
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Score 89; DB 3; Length 33;
Pred. No. 1.2e-07;
0; Mismatches 0; Indels
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publication No. US20030143650A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance B.

APPLICANT: Steward, Lance B.

APPLICANT: Permandez-Salas, Ester

APPLICANT: Permandez-Salas, Ester

APPLICANT: Apki, Kei Roger

TITLE OF INVENTION: Fret Protesse Assays For Botulinum

TITLE OF INVENTION: Serotype A/E Toxins

FILIS REFERENCE: P-AR 4803

CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT APPLICATION NUMBER: US/09/942,024

SOFTWARE: PastSEQ for Windows Version 4.0

SSEQ ID NO 38

LENTH: 33
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Sequence 37, Application US/09942024;
Sequence 37, Application US/09942024;
Publication No. US20030143650A1;
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.;
APPLICANT: Fernandez-Salas, Ester;
APPLICANT: Pernandez-Salas, Ester;
TITLE OF INVENTION: Fret Protease Assays For Botulinum;
TITLE OF INVENTION: Serotype A/E Toxins;
FILE REFERENCE: P-AR 4803;
CURRENT FILLING DATE: 2001-08-28;
NUMBER OF SEQ ID NOS: 96;
NUMBER OF SEQ ID NOS: 96
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.9%; Scilarity 100.0%; P
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18; Conservative 0;
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    18; Conservative
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LENGTH: 33
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Sequence 90, Application US/09942098

Sequence 90, Application US/09942098

Publication No. US20030143651A1

GENERAL HORRANTION:
APPLICANT: Steward, Lance E.
APPLICANT: Remander-Salas, Ester
APPLICANT: Remander-Salas, Ester
TITLE OF INVENTION: Toxins
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT APPLICATION NUMBER: US/09/942,098

SOFTWARE FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 90

LENGTH: 24

TYPE: PRT

TYPE: PRT

CORGANISM: Artificial Sequence
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    DB 3; Length 24;
8.1e-08;
hes 0; Indels
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Sequence 33, Application US/09942024

Sequence 33, Application US/09942024

Publication No. US20030143650A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernander-Salas, Ester
APPLICANT: Render-Salas, Ester
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REPERBANCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PastSEQ for Windows Version 4.0

SEQUID NOS: SOFTWARE: VALUE OF SEQUID NOS: 96
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    Query Match

89.9%; Score 89; DB
Best Local Similarity 100.0%; Pred. No. 8.1
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic peptide NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (0) ...(0)
; OTHER INFORMATION: at the C-terminal US-09-942-098-90
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CORGANISM: Mus musculus
US-09-942-024-33
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Best Local Similarity
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APPLICANT: Stemandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT PAPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SSECTIANT FLING DATE: Anidows Version 4.0
SSEQ ID NO 55
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB 4; Length 33; Pred. No. 1.2e-07; Mismatches 0; Indels
                                          89.9%; Score 89; DB 3; Length 33; 100.0%; Pred. No. 1.2e-07; ive 0; Mismatches 0; Indels
                                                                100.0%; Pred. No. 1.2
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.9%; Score 89; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                         US-10-261-161-55; Sequence 55, Application US/10261161; Publication No. US20040072270A1; GENERAL INFORMATION:
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; ORGANISM: Carassius auratus
US-10-261-161-59
                                              Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
; ORGANISM: Mus musculus
US-10-261-161-55
    US-09-942-098-38
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US-10-261-161-60
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Publication No. US20030143651A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION UNMERE: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 37
LENGTH: 33
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
ITILE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFRENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT APPLICATION NUMBER: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 33
ILENGTH: 33
CRGANISM: Mus musculus
US-09-942-098-33
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89.9%; Score 89; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; IndelR
                                                                                                                                                                                                                                                                                                                       Query Match
89.9%; Score 89; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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US-09-942-098-37
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US-09-942-098-38
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US-10-261-161-59
US-10-261-161-59

Sequence 59, Application US/10261161

Publication No. US20040072270A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Active Control of Co
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89.9%; Score 89; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 60, Application US/10261161

Publication No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Acki, Kei Roger

TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT APPLICATION UNUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FRANCE: PAR 4804

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 60

LENGTH: 33

TYPE: PRT

ORGANISM: Carassius auratus

US-10-261-161-60

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

OY 4 KTRIDEANQRATKHIGG 21
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Search completed: April 3, 2006, 15:57:05 Job time: 94.6606 secs

16 KTRIDEANQRATKMLGSG 33

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4 KTRIDEANORATKMLGSG 21
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US-08-819-286-9
CITY:
STATE:
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103.582 Million cell updates/sec
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Sequence 18,
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Sequence 3
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                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-393-985-18

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US-09-949-016-6311

US-09-949-016-10671

US-09-962-360B-12

US-09-962-360B-12

US-08-743-894B-18

US-08-743-894B-13

US-08-743-894B-30

US-08-743-894B-30
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 1, Ap
Sequence 38, A
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; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
    APPLICANT: Montal, Mauricio
    TITLE OF INVENTION: PEPTIDE INHIBITORS OF
    TITLE OF INVENTION: DELECTION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
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Sequence
Sequence
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
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100.0%; Pred. No. 1.5e-08;
tive 0; Mismatches 0;
US-08-743-894B-2
US-08-743-894B-24
US-08-743-894B-24
US-08-743-894B-28
US-08-743-894B-31
US-08-743-894B-31
US-08-743-894B-34
US-08-743-894B-36
US-08-743-894B-45
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US-08-743-894B-31
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US-08-743-894B-45
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/ABENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/678-5070
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                         GENERAL INCRNATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
TORRESPONDENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Joila
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PEPTIDE INHIBITORS OF
NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
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Pred. No. 2e-08;
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                                                                                                                                                                                                                                                                                                                            ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,642
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: REPTIDE INHIB:
TITLE OF INVENTION: NEUROTRANSMIT:
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                    Sequence 8, Application US/08819286
Patent No. 6169074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619/6/8-5000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
1.RNGTH: 26 amino acids
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Best Local Similarity 100.
Matches 18; Conservative
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COMPUTER READABLE FORM:
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                                                 RESULT 2
US-08-819-286-8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE: US/08/819,286
FILING APPLICATION 514
PRIOR APPLICATION THORMATO:
APPLICATION NUMBER: US 60/013,599
FILING APPLICATION WHORER: US 60/013,599
FILING APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTOMEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISCHATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 34,842
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOW 4:
SEQUENCE CHRARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith CLASSIFICATION: 530
FRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1581.0120001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KTRIDEANQRATKMLGSG 21
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TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: no
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RESULT 7
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Patent No. 6043042

GENERRAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Oulnn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEB: Sterre, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CONTROLLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 89; DB 2; Lengu...
...d. No. 6 Se-08;
0; Indels
                                                                                                                                                                      Length 70;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC COMPATIBLE.
COMPUTER: PAPELINE PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
                                                                                                                                                                    Query Match 89.9%; Score 89; DB 1; Le:
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BEMOIN, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KTRIDEANQRATKMLGSG 21
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                                                                                                                                                                                                                                                                               53 KTRIDBANQRATKMLGSG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10: SEGUIENCE CHARACTERISTICS: LENGTH: 70 amino acids
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                       US-08-760-001-10
                                      LENGTH:
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KTRIDEANQRATKWLGSG 70

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APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteclytic Activities of Clostridi TITLE OF INVENTION: Hearvetoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
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100.0%; Pred. No. 6.5e-08;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               STREET: BC No. No. N.W., Suite 600 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bsmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: James, Benjamin A. F.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Golds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-962-360B-11; Sequence 11, Application US/09962360B; Sequence 11, Application US/09962360B; GENERAL INFORMATION:
Sequence 10, Application US/09534572
Patent No. 6337386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KTRIDEANQRATKMLGSG 21
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TELEFAX: 202----
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.9
Best Local Similarity 100.
Matches 18; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.9%; Score 89; DB 1; Length 206; 100.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                                                 Query Match

89.9%; Score 89; DB 2; Lu
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
LENGTH: 116
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz. Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPRACE: (415) 324-080
TELEPRACE: (415) 324-080
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 KTRIDEANORATKMLGSG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KTRIDEANQRATKMLGSG 21
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Matches 18; Conservative C
                                                                                                                                                                         ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-393-985-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                    LOCATION: 1
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                                                                                                                                                                                                                                          FEATURE:
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189 KTRIDEANQRATKMLGSG 206

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Sequence 6311, Application US/09949016
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
    TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PELING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-00-08
; PRIOR FILING DATE: 2000-09-08
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RESULT 9
US-08-819-286-1
Sequence 1, Application US/08819286
Sequence 1, Application US/08819286
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
89.9%; Score 89; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                               SSEE: Fish & Richardson P.C.
: 4225 Executive Square, Suite 1400
La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILLING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 KTRIDEANORATKWIGSG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
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APPLICANT: James J. Schmidt
APPLICANT: James J. Schmidt
APPLICANT: Waren A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fro
NUMBER OF SEQUENCES: 56
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Heartcoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT PILLIG DATE: 2002-08-19
PRIOR PILLIG DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT A
FEATURE:
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                                                                                                                                                                                         Length 116;
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Best Local Similarity 83.3%; Pred. No. 9.6e-07;
Matches 15; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                         1; Indels
                            NAME/KEY: misc_feature

: LOCATION: 1

: OTHER INNEXTION: Xaa at 1 is S-fluoresceinyl-cysteine

US-09-962-360B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: 1; COTHER INFORMATION: Xaa at 1 is N-fluresceinyl-glycine US-09-962-360B-8
                                                                                                                                                                                     Score 83; DB 2; I
Pred. No. 1.3e-06;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09962360B Patent No. 6762280
                                                                                                                                                                                                                                                                                                                                                                                         98 KTRIDEANQAATKMLGSG 115
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                                                                                                                                                                                                                                                                                                                                   4 KTRIDEANQRATKMLGSG 21
                                                                                                                                                                                         Query Match 83.8%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosk
OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21702-5012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-962-360B-8
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APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid TITLE OF INVENTION: Neurotoxins
FILE REPERENCE: 003/224/SAP
FILE REPERENCE: 003/22-08-19
FILE REPERENCE: 003/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10671, Application US/09949016
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REPRENENCE: CLOOD.307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 10671
; LENGTH: 219
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89.9%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.5e-07;
tive 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6311
LENGTH: 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 KTRIDEANQRATKMLGSG 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 89.9
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
US-09-949-016-10671
                                                                                                                                              ; ORGANISM: Human
US-09-949-016-6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-09-949-016-10671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-962-360B-12
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Gaps

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73.7%; Score 73; DB 1; Length 17; 100.0%; Pred. No. 6.8e-06; tive 0; Mismatches 0; Indels
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Job time : 18.5596 seca
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                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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US-08-743-894B-37
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Sequence 37. Application US/08743894B

Patent No. 5965699

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteclytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn.John Moran-Patent Atty
STREET: USA MRMC - 504 Scott Street
CITY: FORT DEFRICK
STATE:
ARRIAND
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SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: NO. 5955699ember 6, 1996
CLASSIFICATION ATA:
APPLICATION NUMBER:
ATPLICATION NUMBER:
FILING DATE:
ATPORNEY/AGENT INFORMATION:
NAME: CLARICE H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION FOR SEQ ID 19:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
STRANDEDNESS: Single
17PE: amino acid sequence
STRANDEDNESS: Single
17SPE: Linear
US-08-743-894B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: NO. 5965699ember 6, 1996
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-774
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPPLOGY: Linear
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Matches 15; Conservative
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US-08-743-894B-37
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xenopus lae
xenopus lae
brachydanio
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brachydanio
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rattus norv
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xenopus lae
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                                                        April 3, 2006, 15:27:42; Search time 113.431 Seconds (without alignments) 136.837 Million cell updates/sec
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05u0b5
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Q7zve4
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                  2166443 seqs, 705528306 residues
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Q5R505_PONPY
Q640W4_XENLA
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CARAU
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07ZVE4_BRARE
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MACMU
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PANTR
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    1 XMEKTRIDEANQRATKMLGSGX 22
                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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: uniprot_sprot:*
: uniprot_trembl:*
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seq length: 200000000
                                                                                               US-09-942-098-93
99
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         Copyright
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Match
                                                                                                   Title:
Perfect score:
                                                                                                                                         Scoring table:
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Maximum DB s
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No.
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P36976 torpedo mar Q4rep6 tetraodon n Q661d7 brachydanio Q4v9b7 brachydanio Q4v9b6 brachydanio Q87384 loligo peal Q8jis7 xenopus lae Q8jq18 bradyrhizob Q7sf97 neurospora Q9a665 caulobacter Q4p0n6 ustilago ma Q9e1x6 cercopithec P11704 spinacia ol	
SNP25_TORMA Q4REP6_TETNG Q66107_BRARE Q4V9B7_BRARE Q4V9B6_BRARE Q4V9B6_BRARE Q69T354_LOLPE Q61554_KENLA Q89Q18_BRAJA Q75F97_NEUCR Q4P0N6_USTWA Q98156_CAUCR Q4P0N6_USTWA Q98156_9ALPH RPOC2_SPIOL	
2210 1137 2210 1137 2210 2209 2209 2209 2209 2209 2209 2209	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
44 46 46 46 46 46 46 46 46 46 46 46 46 4	
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ALIGNMENTS

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"Cloning of two loci for synapse protein Snap25 in zebrafish:
comparison of paralogous linkage groups suggests loss of one locus in
the mammalian lineage.";
J. Neurosci. Res. 54:563-573 (1998).
BMBJ, AR091593, AAC64289.1; -; mRNA.
BKBP, QBT364; 1144.
SMR; Q93578; 49-122.
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                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(STCI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSDARGO0000020609; Danio rerio.
ZPIN; ZDB-GENE-890526-468; snap25a.
ZPIN; ZDB-GENE-890526-468; snap25a.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
InterPro; IPR002197; HTH Fis.
InterPro; IPR000727; TSARE.
PFam; PP00315; SNAP-25;
InterPro; PR00035; SNAP-25;
InterPro; PR00035; SNARE.
PFam; PP05739; SNARE:
PFam; PP05739; SNARE:
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89.9%; Score 89; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AA; 13616 MW; 50E27DBDB33D958C CRC64;
                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Synaptocome-associated protein 25.1 (Fragment)
Name-snap25a; Synonyms-Snap;
                                                                      124 AA
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTRIDEANQRATKMLGSG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1
                                                                  O93578 BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01590; HTHFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synaptosome.
NON TER
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CONTROLL OF SEATH CONTROLL OF 
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RESULT

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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=snap25a;
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                                                                                                                                                                                                                                                                                                         Matches
    $ $ $ $ $ $ $ $ $ $ $ $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B., Parrad G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Arilla M., Volff M., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals I. Nature 431:946-957(2004).
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TISSUE-Brain parietal lobe;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              ORFNames=GSTENG00022427001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14706, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.9%; Score 89; DB 2; Length 134; 100.0%; Pred. No. 4.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.

, CAAE01014706, CAG03117.1, -, Genomic_DNA.

JENCE 134 AA; 14682 MW; 09109FP243890ABE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AA
                          134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ...
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HSSP; Q8T3S4; 1L4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                          PRT;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9GM34 MACFA PRELIMINARY;
Q9GM347
                       Q4S8B5_TETNG PRELIMINARY;
Q4S8B5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=99883;
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Matches
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OGGM34 MA
AC 09GM34
DT 01-N
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NUCLECTIDE SEQUENCE.

STRAIN-Wild-type; TISSUB-EPF;

KIAUSDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KIACHOL S. F., Zeoberg B. B., Buelcow K.H., Schaefer C.F., Bhat N.K., March L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stander D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rackiquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Recentation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                    ó,
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                    Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                      Pram; Prus/13; SNAKE; 1.
SMART; SM00397; t_SNARE; 1.
PROSTIE; PS50192; T_SNARE; 1.
Hypothetical protein; Synaptosome.
SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nd mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                    89.9%; Score 89; DB 2; Le
100.0%; Pred. No. 4.5e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0019717; C:synaptosome; IEA.
InterPro; IRR000928; SNR-25.
InterPro; IRR000727; T. SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05795; SNAP-25; 1.
SMART; SM00397; t. SNARE; 2.
PROSITE; PSS0192; T. SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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SMR; Q6PC84; 1-77, 123-196.
ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GG:0019717; C:8ynaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR00077; T_SNARE.
Pfam; PP00935; SNAP-25; 1.
Pfam; PP05739; SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 KTRIDEANQRATKMLGSG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEPC84 BRARE PRELIMINARY;
QEPC84
05-JUL-2004 (TEMBLFEl. 27,
05-JUL-2004 (TEMBLFEl. 27,
05-JUL-2004 (TEMBLFEl. 27,
                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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us-09-942-098-93.rup

186 KTRIDEANQRATKMLGSG 203

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4 KTRIDEANQRATKMLGSG 21

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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                           ö
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fam; PF05739; SNARE; 1.

Fam; PF05739; SNARE; 1.

SMART; SM00397; L. SNARE; 2.

PROSITE; PS50192; T SNARE; 2.

Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome. t-SNARE coiled-coil homology 1.

t-SNARE coiled-coil homology 2.

t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the nerve terminal.
--- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, a granule cells of the cerebellum.
--- SIMILARITY: Belongs to the SNAP-25 family.
--- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 92 Cys-rich.
77 77 N-linked (GlcNAc. ..) (Potential)
185 185 N-linked (GlcNAc. ..) (Potential)
203 AA; 22664 MW; 8DFBBEDBED37D6D7 CRC64;
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Risinger C., Larhammar D.; "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.9%; Score 89; DB 1; Length 203; 100.0%; Pred. No. 6.4e-06; tive 0; Mismatches 0; Indels
                                         Length 198;
         22209 MW; 8FED5099A00E1EC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad. Sci. U.S.A. 90:10598-10602(1993).
                                     Hactin 89.9%; Score 89; DB 2; Lk Local Similarity 100.0%; Pred. No. 6.3e-06; les 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 25B (SNAP-25B)
                                                                                                                                                                                                                                    203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, 1.22976; AAA16538.1; -; mRNA.
PIR, 150481; 150481.
HSSP; P13795; 1.8FC.
SMR; P36978; 7-82, 128-201.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T. SNARE.
Pfam; PF00835; SNAP-25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94068448; PubMed=8248151;
                                                                                                                                                181 KTRIDEANQRATKMLGSG 198
                                                                                                               4 KTRIDEANORATKWLGSG 21
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
              198 AA;
Synaptosome.
                                                                                                                                                                                                                                      CARAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl.
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Best Local S:
Matches 18
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CARBOHYD
SEQUENCE
              SEQUENCE
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                                              Query Match
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P3697B;
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"Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinoperygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                Brachydanio rezio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99057281; PubMed=9843147;
DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Wild-type; TISSUB=Bye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colline F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                01-NOV-1998 (T-EMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Synaptosome-associated protein 25.2.
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Pred. No. 6.4e-06;
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203 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Neurosci. Res. 54563-573 (1998).

EMEL; AF091594; AAC64290.1; -; mRNA.

EMSP; P60881; JuTH.

SMR; O93579; 7-82, 128-201.

ZFIN; ZDB-GENE-980526-392; snap25b.

GO; GO:0019717; C:synaptrosome; IEA.

InterPro; IPR000928; SNAP-25.

InterPro; IPR000727; T_SNARE.

Pfam; PF00835; SNAP-25; 1.

FAM; SMORY; SMORS; 1.

SMARY; SMO0397; L_SNARE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synaptosome-associated protein 25 b
PRT;
                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KTRIDEANORATKMLGSG 21
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O93579 BRARE PRELIMINARY;
093579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Larhammar D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Q6PC54_BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SO OR REPLY SERVING TO THE SERVING THE SER
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Local Similarity nes 18; Conserv

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NCBI_TaxID=8164;
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Q705J6_LA
           SO DE REPORTED DE LA PROPERTICIO DELLA PROPERTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ሯ
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapheton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bromstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.W., Wardey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Willianon D.K., Muzny D.M., Schmetz D., Dickson M.C., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schehn J.E., Jones S.J.M., Marra M.A.; Human and mouse cDNA sequences.", The mod mod sequences.", The mod sequences.", The mod mod sequences.", The mod sequences.", The mod sequences.", The mod sequences.", The mod seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neoperygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
-!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
-!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nerve terminal. SIMP-25 family. SIMILARITY: Belongs to the SNAP-25 family. SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
Local Similarity 100.0%; Pred. No. 6.4e-06;
Les 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC059469; AMF59499.1; -; mRNA.
SMR; QEPC54; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 AA; 22693 MW; 48D7590DD0C1179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MN-1994 (Rel. 47, Last amoutation update)
Synaptosomal-associated protein 25A (SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA
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MEDLINE-94068448; PubMed-8248151;
Risinger C., Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 KTRIDEANORATKWIGSG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Wild-type, TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (OCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SN25A CARAU
P36977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synaptosome
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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A Chen K., Huang X.H.;
A Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
B Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
R SMR; Q705J6; 7-83, 129-202.
R SMR; Q705J6; 7-83, 129-202.
R GO; G0:0003700; F:transcription factor activity; IEA.
R GO; GO:0000355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000328; SNAP-25.
DR InterPro; IPR00329; SNAPE.
DR Ffam; PF00339; SNAPE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Buteloostomi;
Actinopterygii, Neopterygii; Teleostei, Buteleostei, Neoteleostei, Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                 R EMBL; L22973; AAA16537.1; -; mRNA.

R HSSP; P13795; L1796.

R RSSP; P3697; 7-83, L29-202.

R InterPro; IPR000928; SNAP-25.

R InterPro; IPR000727; T_SNARE.

R Pfam; PF06739; SNARE; 1.

R Pfam; PF06739; SNARE; 2.

R PROSITE; PS50192; T_SNARE; 2.

R PROMAIN 138 200 t_SNARE coiled-coil homology 1.

I DOMAIN 138 200 t_SNARE coiled-coil homology 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cys-rich.
458BBECFCFC09189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Synaptosomal-associated protein 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.9%; Score 89; DB 1; Le
100.0%; Pred. No. 6.5e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 KTRIDEANQRATKMLGSG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 KTRIDEANORATKMLGSG 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 92 C
204 AA; 22843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q705J6 LATJA PRBLIMINARY;
Q705J6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moronidae; Lateolabrax.
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                                                             01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
8ynaptosomal associated protein (SNAP).
Name=snap25a; Synonyms=CTTDARPRO000005563; ORFNames=DKEYP-8F4.6-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio Retazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
Name-snap25a; Synonyms-OTTDARP0000005690; ORFNames-DKEYP-8F4.6-002;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Releostei; Ostariophysi; Cypriniformes;
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89.9%; Score 89; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; Bx465184; CAH69032.1; -; Genomic_DNA.
EMBL; Bx470246; CAL3360.1; -; Genomic_DNA.
EMBL; Bx470246; CAH69032.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lovell J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lovell J.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donaldson S.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ da Bylaitted (DEC-2004) to the EMBL/GenBank/DDBJ da EMBL; BX460246; CAI21359.1; -; Genomic_DNA.
EMBL; BX470246; CAI21359.1; -j Genomic_DNA.
EMBL; BX470246; CAI69031.1; JOINED; Genomic_DNA.
EMBL; BX465184; CAI21359.1; JOINED; Genomic_DNA.
SMR; OSTZG6; 7-83, 129-202.
ENSEMD1; ENSDARG000002c609; Danio rerio.
                           204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZETIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptcsome; IEA.
Interpro; IPRO00928; SNAP-25.
Interpro; IPRO00727; T SNARE.
Pfam; PPO0835; SNAP-25; 1.
SNART; SM0039; L SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 KTRIDEANQRATKMLGSG 204
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QSTZ65;
                 QSTZ66_BRARE PRELIMINARY;
QSTZ66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSTZ65_BRARE
BRARE
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05TZ66
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Event-Alternative splicing, Named isoforms=2, Comment=Isoforms differ by the usage of two alternative homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Supers CHICK STANDARD; PRT; 206 AA.

P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
P601-JAN-1990 (Rel. 13, Last asseciated sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Synaptosomal-associated protein 15 (SNAP-25) (Synaptosomal-associated
25 kDa protein) (Super protein) (SUP).
Name-SNAP25; Synonyma-SNAP;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity).
SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STXIA. This complex binds CPLXI. Interacts with TRIM9, RIMSI and SYRAP55BP. Binds STXEP6. Found in a ternary complex with STXIA and VAMM8 (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of the chicken gene for SNAP-25 reveals duplicated exon "Structure of the chicken of the protein.";
J. Mol. Biol. 233:67-76(1993).
-!- FUNCTION: L-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
STRAIN=White leghorn; TISSUE=Retina;
MEDLINE=91126080; PubMed=1992470;
Catsicas S., Larhammar D., BlomqVist A.G., Sanna P.P., Milner R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression of a conserved cell-type-specific protein in nerve terminals coincides with synaptogenesis."; Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                             Length 204;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                         204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
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                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0;
EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA.SMR; Q5TZ65; 7-83, 129-202.
Ensembl; ENSDARG00000020609; Danio rerio.
ZFIN; ZDB-GENE-980526-468; snap25a.
                                                                         GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000228; SNAP-25.
InterPro; IPR000727; T. SNARE.
Pfam; PF00835; SNAP-25; 1.
Fram; PF05739; SNARE; 1.
SWART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93389738; PubMed=8377193;
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                                                                                                                                                                                                                                                                                                                                                            IsoId=P60878-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                        4 KTRIDEANQRATKMLGSG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=SNAP-25a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                 Synaptosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson M.C
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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MEDLINE=94333829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2; Zhao N., Hashida H., Takahashi N., Sakaki Y.; "Cloning and sequence analysis of the human SNAP25 cDNA."; "Gene 145:313-314(1994).
                                        MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
                                                                   Bark I.C., Wilson M.C.; "Human CDNA Clones encoding two different isoforms of the nerve terminal protein SNAP-25."; Gene 139:291-292(1994).
NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B)
                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                     NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A)
                                                                                                                                                                                                             rissum-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogers
  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Cleavage (by BONT/E) (By similarity).
Chesvage (by BONT/E) (By similarity).
Phosphoserine (By similarity).
ERIEEGMDQINKDMXEAEKNLTDLGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $\text{SNP25}$ HUMAN STANDARD; PRT; 206 AA. $\text{P60860}$; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45; $\text{P60860}$; P13795; P36974; P70558; Q81XK3; Q96FM2; Q9BR45; $\text{O1-JAN-1990}$ (Rel. 13, Created) $\text{Carted}$; Carted $\text{O1-FB-1991}$ (Rel. 17, Last sequence update) $\text{13-SEP-2005}$ (Rel. 48, Last annotation update) $\text{Synaptcosomal-associated}$ protein 25 (SNAP-25) (Synaptcosomal-associated $\text{Synaptcosomal-associated}$ \text{Name=SNAP25}$; Synonyms=SNAP$; Name=SNAP25; Synonyms=SNAP$; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMNHINQDMKEAEKNLKDLGKCCGLFI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                     -1- PTM: Palmitoylated (By similarity).
-1- SIMILARITY: Belongs to the SNAP-25 family.
-1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Repeat; Synaptosome.

19 81 t-SNARE coiled-coil homology 1.

COWAIN 10 202 t-SNARE coiled-coil homology 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00035; SNAP-25; 1.
SMART; SN00397; T_SNARE; 1.
SMART; SN00397; T_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.9%; Score 89; DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
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                                                                                                                                                                                                                                          EMBL; M57957; AAA49072.1; -; mRNA.
EMBL; L09254; AAA49070.1; -; Genomic DNA.
EMBL; L09254; AAA49070.1; JOINED; Genomic DNA.
EMBL; L09255; AAA49070.1; JOINED; Genomic DNA.
EMBL; L09259; AAA49070.1; JOINED; Genomic DNA.
EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
EMBL; L09250; AAA49070.1; JOINED; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA49071.1; -; Genomic_DNA.
AAA49071.1; JOINED; Genomic_DNA.
AAA49071.1; JOINED; Genomic_DNA.
AAA49071.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L09259; AAA49071.1; JOINED; Genomic_DNA
L09252; AAA49071.1; JOINED; Genomic_DNA
L09250; AAA49071.1; JOINED; Genomic_DNA
L09250; AAA49071.1; JOINED; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNAP-25a).
/FTId=VSP_010018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 KTRIDEANQRATKMLGSG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A37861; A37861.
SMR; P60878; 7-83, 131-204.
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L09254;
L09257;
L09259;
                                                                                                                                                                                                                                                                                                                                                                                                                                            L09253;
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                                                                                                                                                                                                           removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
EMBL;
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EMBL;
EMBL;
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Matches
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  SOLUTION TO THE STATE ST
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RX NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX Deloukas P., Matchews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.M., Beard L.M., Beare D.M.,

RA Bailey O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Chapman J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

RA Chapman J.C., Deadman R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Capley V.E., Calffiths M.N.D., Gwilliam R., Hall R.E.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Matrin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikkin J.C., Nickerson T.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikkin J.C., Nickerson T.,

RA Skuce C.D., Smith M.L., Socherlund C., Steward C.A., Sulston J.E.,

RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,

Whitehead S.L., Whittaker P., Willey D.L., Milliams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whitehead T., Durbin R.M., Bentley D.R., Beck S.,

Wanner R. W. Poorer R. Durbin R.M., Bentley D.R., Beck S.,

RA Williaming L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

Ranner R. W. Bentley P.W., Bentley R., Beck S.,

Ranner R. W. Walley P. W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

Ranner R. W. Bentley D. W., Ranner T. Bentley D.R., R. Willey D. W., Will
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TISSUB-Skeletal muscle;
MEDLINE-96332494; PubMed=8760387;
Magadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
Ward C.W.;
                                                                                                                                                                                                                                                                                                                                                                                "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 317:945-954 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 414:865-871(2001).
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Ensembl;
             removed
                   HGNC;
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Pfam; PF00835; SNAP-25; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                           WITH STXIA; CPLX1 AND VAMP2, AND NWR ANALYSIS.
WITH STXIA; CPLX1 AND VAMP2, AND NOTE OF ANALYSIS.
WITH STXIA; CPLX1 AND VAMPE OF THE COMPLEX OF THE COMPLEX OF THE CPLX ANALYSIS.

SYNDATIC FUNCTION OF SPECIFIC NEURONAL FOLE IN THE PROTECTION OF SPECIFIC NEURONAL SYSPECTION.
WITH STXIA; THIS COMPLEX DATASE CONTENTING SYMAPS.

SUBUNIT: PART OF THE SNARE CONE COMPLEX CONTENTING SYMAPS.
AND STXIA AND WARPS (BY SIMIS CPLXI. INTERCACES WITH TRIMS), WITH SYMAPS.
SYNIA AND WARPS (BY SIMISTIA).
                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=2;
Comment=Isoforms differ by the usage of two alternative
homologous exons (5a and 5b) which encode for positions 56 to 94
and differ only in 9 positions out of 39;
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBIUH5:HIP14; NbExp=1; IntAct=EBI-524785, EBI-524753; ALTERNATIVE PRODUCTS:
                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL023913; CAC34534.1; -; mRNA.

REMBL; AL023913; CAC34534.1; -; Genomic_DNA.

REMBL; AL023913; CAC34535.1; -; Genomic_DNA.

REMBL; AL023913; CAC34535.1; -; Genomic_DNA.

REMBL; AL023913; CAB42860.1; -; Genomic_DNA.

REMBL; EMD1; AL023913; CAB42860.1; -; Genomic_DNA.

REMBL; ES735; 153735.

PIR; IC7923; IC7923.

PIR; IC7923; IC7923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mbl; ENSG00000132639; Homo sapiens; HGNC:11132; SNAP25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKIL; K.ray; C=11-80, D=141-203.
IXTG; X-ray; B=146-204.
P60880; 7-83, 131-204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L19760; AAC37545.1; -; MRNA.
EMBL; L19761; AAC37546.1; -; MRNA.
EMBL; D21267; BAA22370.1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=SNAP-25a;
Isold=P60880-2, P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P60880-1, P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=SNAP-25b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IntAct; P60880; -
                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION:
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                                                                                                                                                                                                                      Cys-rich.
Cleavage (by BONT/E).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
ERIEEGMDQINKDMKEAEKNLTDLGKFCGLCV -> DRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP25 MACMU STANDARD; PRT; 206 AA.

ID SNP25 MACMU STANDARD; PRT; 206 AA.

AC P60877; P13795; P36974; P70559; Q81XK3; Q96FM2; Q9BR45;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated GN Name-SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STXIA. This complex binds CPLX1. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with STXIA and VAMP8 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                 GMNHINQDMKEAEKNLKDLGKCCGLFI (in isoform SNAP-25a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Hippocampus;
Jensem M.G., Smith L.A.;
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: t-SNARE involved in the molecular regulation of
neurotransmitter release. May play an important role in the
synaptic function of specific neuronal systems. Associates with
proteins involved in vesicle docking and membrane fusion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: Palmitoylated (By similarity). SIMILARITY: Belongs to the SNAP-25 family. SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Pfam; Provocas;
Pfam; Provocas;
SMART; SM00397; t_SNARE; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50132; T_SNARE; 2.
PROSITE; PS50132; T_SNARE; 2.
PROSITE; PS60132; T_SNARE; 2.
PAINITATE; Phosphorylation; Repeat; Synaptosome.
DOWAIN 19 81 t_SNARE coiled-coil homology 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.9%; Score 89; DB 1; Length 206; 100.0%; Pred. No. 6.5e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 82
142 201
202 202
206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_006186
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SMR; P60877; 7-83, 131.204.
INCEPPO; IPR000928; SNAP-25.
INCEPPO; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 KTRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KTRIDEANQRATKMLGSG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
                                                                                                                                                                                              DOMAIN
COMPBIAS
SITE
                                                                                                                                                                                                                                                                                                                   MOD_RES
VARSPLIC
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HELIX
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STRAIN-C57BL/6J; TISSUE-Medulla oblongata;

MEDLINE-22254681; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE-22254681; PubMed=12466851; DOI=10.1038/nature01266;

A Nikaido I., Osato N., Saito R., Surauki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T., Radalarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Dagani T.A., Fletcher C.F., Fortreat A., Frazer K.S., Gasterland T.A., Fletcher C.F., Fortreat A., Frazer K.S., A Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Aknai A., Kurochkin I.V., Lee Y., Lehard B., Lyons P.A., Nagalott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
                                                                                                                                                                                                                                                                                                                                         SNP55 MOUSE STANDARD; PRT; 206 AA.
P60879; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
P00879; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
P13-NP-1990 (Rel. 13, Lact annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated 25 kDa protein) (SUP).
Name-Snap25; Synonyms-Snap;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C;
MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
Bloom F.E., Wilson M.C.;
"The identification of a novel synaptosomal-associated protein, SNAP-25, differentially expressed by neuronal subpopulations.";
J. Cell Biol. 109:3039-3052(1989).
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                     Cleavage (by BONT/E) (By similarity). Phosphothreonine (By similarity). Phosphoserine (By similarity). FBED2B082A4CB6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ILS, and ISS;

BEDLINES-1553810. PubMed=11471062; DOI=10.1007/800335-001-1001-x;

Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,

Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;

"High-throughput sequence identification of gene coding variants

within alcohol-related GTLs.";

Mamm. Genome 12:657-663 (2001).
                                                                                                                                                                                                                    ö
                      SMART, SM00397; t_SNARE, 2.
PROSITE; PS50192; T_SNARE; 2.
Colled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
                                                                              t-SNARE coiled-coil homology 1.
                                                                                                                                                                                       DB 1; Length 206;
6.5e-06;
hes 0; Indels
                                                                                                                                                                                        89.9%; Score 89; DB 100.0%; Pred. No. 6.5 Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
                                                                                                           Cys-rich.
                                                                                                                                                                                                                                                                     189 KTRIDEANQRATKMLGSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muroidea; Muridae; Murinae; Mus
                                                                            81 t-
202 t-
92 CY
181 CI
138 Ph
187 Ph
                                                                                                                                                                                                                                               4 KTRIDEANQRATKMLGSG 21
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
                                                                                                                                                                                        Query Match 89.9
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                    Synaptosome.
                                                                                            DOMAIN
                                                                                                                                    MOD_RES
MOD_RES
SEQUENCE
                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                MOUSE
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 STITIES
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RA Bellovsky N. Pilais R., Fontius Jul., Of D., Ramachandran S., Ra Andalin., Red Linds R., Fontius Jul., Section W. Stinada R., Sindalin., Red Linds R., Stinada R., Sindalin., Red Linds R., Section W. S., Strang H. S., Stinada R., Shinada R., Sh
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-i- PTM: Palmitoylated (By similarity).
-i- SIMILARITY: Belongs to the SNAP-25 family.
-i- SIMILARITY: Contains 2 t-SNARB coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

89.9%; Score 89; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           EMBL; M22012; AAA61741.1; -; MRNA.
EMBL; AF483516; AAL90790.1; -; MRNA.
EMBL; AF483517; AAL90791.1; -; MRNA.
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4 KTRIDEANORATKMLGSG 21

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Search completed: April 3, 2006, 15:46:24 Job time : 114.431 secs

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